


044599422 07 DEC 2001

J007 Rec'd PCT/PTO 07 DEC 2001

FORM PTO-1390 (Modified) (REV 5-93)		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEY'S DOCKET NUMBER	
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371				029029-0101	
				U.S. APPLICATION NO. (If known, see 37 CFR 1.51) Unassigned 09/980862	
INTERNATIONAL APPLICATION NO. PCT/DE00/01873		INTERNATIONAL FILING DATE 06/08/2000		PRIORITY DATE CLAIMED 06/08/1999	
TITLE OF INVENTION MUTEINS OF THE BILIN-BINDING PROTEIN					
APPLICANT(S) FOR DO/EO/US Steffen SCHLEHUBER					
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:					
<p>1. <input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.</p> <p>2. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.</p> <p>3. <input type="checkbox"/> This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).</p> <p>4. <input checked="" type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19<sup>th</sup> month from the earliest claimed priority date.</p> <p>5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2))</p> <p style="margin-left: 20px;"><input type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau).</p> <p style="margin-left: 20px;"><input checked="" type="checkbox"/> has been transmitted by the International Bureau.</p> <p style="margin-left: 20px;"><input type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US)</p> <p>6. <input checked="" type="checkbox"/> A translation of the International Application into English (35 U.S.C. 371(c)(2)).</p> <p>7. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))</p> <p style="margin-left: 20px;"><input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau).</p> <p style="margin-left: 20px;"><input type="checkbox"/> have been transmitted by the International Bureau.</p> <p style="margin-left: 20px;"><input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired.</p> <p style="margin-left: 20px;"><input checked="" type="checkbox"/> have not been made and will not be made.</p> <p>8. <input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).</p> <p>9. <input type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).</p> <p>10. <input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).</p> <p>11. <input type="checkbox"/> Applicant claims small entity status under 37 CFR 1.27.</p>					
Items 12. to 17. below concern other document(s) or information included:					
<p>12. <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98.</p> <p>13. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.</p> <p>14. <input checked="" type="checkbox"/> A FIRST preliminary amendment.</p> <p style="margin-left: 20px;"><input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment.</p> <p>15. <input type="checkbox"/> A substitute specification.</p> <p>16. <input type="checkbox"/> A change of power of attorney and/or address letter.</p> <p>17. <input checked="" type="checkbox"/> Other items or information: Paper copy of Sequence Listings and Application Data Sheet</p>					

JC10 Rec'd PCT/PTO 07 DEC 2001

U.S. APPLICATION NO. (If known, see 37 CFR 1.59) <b>Unassigned 09/980862</b>		INTERNATIONAL APPLICATION NO. <b>PCT/DE00/01873</b>		ATTORNEY'S DOCKET NUMBER <b>029029-0101</b>	
18. <input checked="" type="checkbox"/> The following fees are submitted:				<b>CALCULATIONS</b>	
Basic National Fee (37 CFR 1.492(a)(1)-(5): Search Report has been prepared by the EPO or JPO.....\$890.00					
International preliminary examination fee paid to USPTO (37 CFR 1.482) .....\$710.00					
No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)) .....\$740.00					
Neither international preliminary examination fee (37 CFR 1.482) nor International search fee (37 CFR 1.445(a)(2)) paid to USPTO ..... \$1,040.00					
International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4) .....\$100.00					
<b>ENTER APPROPRIATE BASIC FEE AMOUNT =</b>				<b>\$890.00</b>	
Surcharge of \$130.00 for furnishing the oath or declaration later than 20 Months from the earliest claimed priority date (37 CFR 1.492(e))				<b>\$0.00</b>	
Claims	Number Filed		Included in Basic Fee	Extra Claims	Rate
Total Claims	16	-	20	= 0	× \$18.00
Independent Claims	2	-	3	= 0	× \$84.00
Multiple dependent claim(s) (if applicable)				\$280.00	
<b>TOTAL OF ABOVE CALCULATIONS =</b>				<b>\$890.00</b>	
Reduction by ½ for filing by small entity, if applicable.				<b>\$0.00</b>	
<b>SUBTOTAL =</b>				<b>\$890.00</b>	
Processing fee of \$130.00 for furnishing English translation later the 20 months from the earliest claimed priority date (37 CFR 1.492(f)).				+	
<b>TOTAL NATIONAL FEE =</b>				<b>\$890.00</b>	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property +				<b>\$0.00</b>	
<b>TOTAL FEES ENCLOSED =</b>				<b>\$890.00</b>	
				Amount to be: \$	
				refunded	
				charged \$	
<p>a. <input checked="" type="checkbox"/> A check in the amount of \$890.00 to cover the above fees is enclosed.</p> <p>b. <input type="checkbox"/> Please charge my Deposit Account No. <u>19-0741</u> in the amount of \$_____ to the above fees. A duplicate copy of this sheet is enclosed.</p> <p>c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>19-0741</u>. A duplicate copy of this sheet is enclosed.</p>					
<p>NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.</p>					
<p>SEND ALL CORRESPONDENCE TO:</p> <p><b>Foley &amp; Lardner</b> Customer Number: 22428</p>  <p><b>22428</b></p> <p>PATENT TRADEMARK OFFICE</p>					
<p><i>Philip J. Articola</i> SIGNATURE <i>Philip J. Articola</i> NAME / <b>STEPHEN B. MAEBIUS</b></p> <p>REGISTRATION NUMBER 35,264 <i>Reg. No. 38,819</i></p>					

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Applicants: Steffen Schlehuber

Entitled: Muteins of the Bilin-Binding Protein

Serial No.: To be assigned

Date Filed: Concurrently

**PRELIMINARY AMENDMENT**

Commissioner for Patents  
Washington, D.C. 20231

Sir:

Prior to examination of the present application, Applicant's respectfully requests that the above-identified application be amended as follows:

**In the Claims:**

Please cancel the second claim 15 without prejudice or disclaimer

In accordance with 37 C.F.R. § 1.121(c) (3), please substitute for pending claims 3, 5-8, 13, 15, and 17 with the following clean version of the claims. The changes to these claims are shown explicitly in the attached "Marked Up Version of Claims."

3. (Amended) The polypeptide according to claim 1, characterized in that it carries, in comparison with the bilin-binding protein, at least one of the amino acid substitutions selected from Glu(28)->Gln, Lys(31)->Ala, Asn(34)->Asp, Ser(35)->His, Val(36)->Ile, Glu(37)->Thr, Asn(58)->Arg, His(60)->Ser, Ile(69)->Ser, Leu(88)->Tyr, Tyr(90)->Ile, Lys(95)->Gln, Asn(97)->Gly, Tyr(114)->Phe, Lys(116)->Ser, Gln(125)->Met, and Phe(127)->Leu.

5. (Amended) The polypeptide as claimed in claim 1, characterized in that it carries at least one label group, selected from enzymatic label, radioactive label, fluorescent

label, chromophoric label, (bio) luminescent label or label containing haptens, biotin, metal complexes, metals or colloidal gold.

6. (Amended) Fusion proteins of polypeptides according to claim 1, characterized in that an enzyme, another protein or a protein domain, a signal sequence and/or an affinity peptide is fused to the amino terminus of the polypeptide in an operable manner.

7. (Amended) Fusion proteins of polypeptides according to claim 1, characterized in that an enzyme, another protein or a protein domain, a targeting sequence and/or an affinity peptide is fused to the carboxy terminus of the polypeptide in an operable manner.

8. (Amended) A nucleic acid, characterized in that it comprises a sequence coding for a mutein or a fusion protein of a mutein of the bilin-binding protein according to claim 1.

13. (Amended) The method according to claim 10, wherein the enrichment of step (d) is carried out by forming a complex of the muteins with the digoxigenin group and subsequently dissociating the complex.

15. (Amended) A method for preparing a mutein or a fusion protein of a mutein of the bilin-binding protein according to claim 1 for preparing a mutein which is obtainable by:

(a) subjecting the bilin-binding protein to random mutagenesis at at least one of the sequence positions 28, 31, 34, 35, 36, 37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125, and 127,

(b) enriching resulting muteins with binding affinity for the digoxigenin group by selection and isolating said muteins,

(c) subjecting the muteins obtained in step (b) to another random mutagenesis at at least one of the sequence positions, 28, 31, 34, 35, 36, and 37, and

(d) again enriching the resulting muteins by selection and isolating said muteins,

characterized in that the nucleic acid coding for the mutein or the fusion protein of a mutein of the bilin-binding protein is expressed in a bacterial or eukaryotic host cell and the polypeptide is obtained from the cell or the culture supernatant.

17. (Amended) A method for detecting the digoxigenin group, wherein a mutein of the bilin-binding protein or a fusion protein of a mutein of the bilin-binding protein according to claim 1 or a mutein which is obtainable according to a method which is obtainable by:

- (a) subjecting the bilin-binding protein to random mutagenesis at at least one of the sequence positions 28, 31, 34, 35, 36, 37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125, and 127,

- (b) enriching resulting muteins with binding affinity for the digoxigenin group by selection and isolating said muteins,

- (c) subjecting the muteins obtained in step (b) to another random mutagenesis at at least one of the sequence positions, 28, 31, 34, 35, 36, and 37, and

- (d) again enriching the resulting muteins by selection and isolating said muteins,

which is brought into contact with digoxigenin or with conjugates of digoxigenin under conditions suitable for effecting binding of the mutein to the digoxigenin group, and the mutein or the fusion protein of the mutein is determined.

**REMARKS**

Applicant respectfully requests that the foregoing amendments be made prior to examination of the present application.

Respectfully submitted,

Dated: December 7, 2001

FOLEY & LARDNER  
3000 K Street, N.W., Suite 500  
Washington, D.C. 20007-5109  
Telephone: (202) 672-5569  
Facsimile: (202) 672-5399  
E-mail: Smaebius@foleylaw.com

By Philip J. Artiola <sup>Reg. No.</sup> 38,819  
for/ Stephen B. Maebius  
Attorney for Applicant  
Registration No. 35,264

**MARKED UP VERSION OF AMENDED CLAIMS**

3. (Amended) The polypeptide according to claim 1[or 2], characterized in that it carries, in comparison with the bilin-binding protein, at least one of the amino acid substitutions selected from Glu(28)->Gln, Lys(31)->Ala, Asn(34)->Asp, Ser(35)->His, Val(36)->Ile, Glu(37)->Thr, Asn(58)->Arg, His(60)->Ser, Ile(69)->Ser, Leu(88)->Tyr, Tyr(90)->Ile, Lys(95)->Gln, Asn(97)->Gly, Tyr(114)->Phe, Lys(116)->Ser, Gln(125)->Met, and Phe(127)->Leu.

5. (Amended) The polypeptide as claimed in [one or more the claims 1 to 4] claim 1, characterized in that it carries at least one label group, selected from enzymatic label, radioactive label, fluorescent label, chromophoric label, (bio) luminescent label or label containing haptens, biotin, metal complexes, metals or colloidal gold.

6. (Amended) Fusion proteins of polypeptides according to [one or more of claims 1 to 5] claim 1, characterized in that an enzyme, another protein or a protein domain, a signal sequence and/or an affinity peptide is fused to the amino terminus of the polypeptide in an operable manner.

7. (Amended) Fusion proteins of polypeptides according to [one or more of claims 1 to 6] claim 1, characterized in that an enzyme, another protein or a protein domain, a targeting sequence and/or an affinity peptide is fused to the carboxy terminus of the polypeptide in an operable manner.

8. (Amended) A nucleic acid, characterized in that it comprises a sequence coding for a mutein or a fusion protein of a mutein of the bilin-binding protein according to [one or more of claims 1 to 7] claim 1.

13. (Amended) The method according to [any of claims 10 to 12] claim 10, wherein the enrichment of step (d) is carried out by forming a complex of the muteins with the digoxigenin group and subsequently dissociating the complex.

15. (Amended) A method for preparing a mutein or a fusion protein of a mutein of the bilin-binding protein according to [one or more of claims 1 to 7 or] claim 1 for

preparing a mutein which is obtainable by: [according to a method according to one or more of claims 10 to 14,]

(a) subjecting the bilin-binding protein to random mutagenesis at at least one of the sequence positions 28, 31, 34, 35, 36, 37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125, and 127,

(b) enriching resulting muteins with binding affinity for the digoxigenin group by selection and isolating said muteins,

(c) subjecting the muteins obtained in step (b) to another random mutagenesis at at least one of the sequence positions, 28, 31, 34, 35, 36, and 37, and

(d) again enriching the resulting muteins by selection and isolating said muteins,

characterized in that the nucleic acid coding for the mutein or the fusion protein of a mutein of the bilin-binding protein is expressed in a bacterial or eukaryotic host cell and the polypeptide is obtained from the cell or the culture supernatant.

17. (Amended) A method for detecting the digoxigenin group, wherein a mutein of the bilin-binding protein or a fusion protein of a mutein of the bilin-binding protein according to [one or more of claims 1 to 7] claim 1 or a mutein which is obtainable by: [according to a method according to one or more of claims 10 to 14]

(a) subjecting the bilin-binding protein to random mutagenesis at at least one of the sequence positions 28, 31, 34, 35, 36, 37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125, and 127,

(b) enriching resulting muteins with binding affinity for the digoxigenin group by selection and isolating said muteins,

(c) subjecting the muteins obtained in step (b) to another random mutagenesis at at least one of the sequence positions, 28, 31, 34, 35, 36, and 37, and

(d) again enriching the resulting muteins by selection and isolating said muteins,



Atty. Dkt. No. 029029/0101

which is brought into contact with digoxigenin or with conjugates of digoxigenin under conditions suitable for effecting binding of the mutein to the digoxigenin group, and the mutein or the fusion protein of the mutein is determined.

Muteins of the bilin-binding protein

The present invention relates to muteins of the bilin-binding protein which are capable of binding digoxigenin and to fusion proteins of such muteins, to methods for preparing muteins of this kind and their fusion proteins and also to the use thereof for detecting or binding biomolecules labeled with digoxigenin.

10

In molecular biology, the digoxigenin group is these days a very common instrument for nonradioactive detection of nucleic acids, proteins and other biomolecules. For this purpose, the biomolecule is, mostly covalently, modified with a reactive digoxigenin derivative, thus allowing subsequent detection of the molecule using an antibody directed against the digoxigenin group or a conjugate of an appropriate antibody fragment and a reporter enzyme, according to generally used methods in biochemistry.

20

The skilled worker knows quite a number of reactive digoxigenin derivatives, which are in part also commercially available. For example, digoxigenin-3-O-methylcarbonyl- $\epsilon$ -aminocaproic acid N-hydroxysuccinimide ester (DIG-NHS), digoxigenin-3-O-succinyl- $\epsilon$ -aminocaproic acid N-hydroxysuccinimide ester and 3-amino-3-deoxydigoxigenin-hemisuccinimide succinimidyl ester are suitable for covalent coupling to proteins, in particular to the amino groups of exposed lysine side chains. Using 3-iodoacetyl-amino-3-deoxydigoxigenin it is possible to label especially thiol groups in proteins or in other biomolecules in a selective manner with the digoxigenin group. It is possible to couple synthetic oligodeoxynucleotides to the same reactive digoxigenin derivatives, as long as they have been equipped with suitable free amino or thiol groups during synthesis.

35

In addition, cis-platinum complexes of digoxigenin derivatives (DIG Chem-Link reagent) or digoxigenin derivatives containing carbodiimide groups (disclosed  
5 in the European patent specification EP 0 806 431 A2) are suitable for the direct labeling of nucleic acids. Alternatively, it is possible in the case of deoxyribonucleic acids to label said deoxyribonucleic acids during a template-dependent enzymatic synthesis  
10 with the aid of a DNA polymerase and a deoxynucleotide triphosphate coupled to the digoxigenin group, for example digoxigenin-11-dUTP, digoxigenin-11-ddUTP or digoxigenin-16-dATP. Analogously, digoxigenin-11-UTP is suitable for incorporation into enzymatically  
15 synthesized RNA. Moreover, it is possible to label oligodeoxynucleotides with the digoxigenin group directly in the automated DNA synthesis by using suitable activated building blocks, for example so-called "virtual nucleotides". Digoxigenin group-coupled  
20 nucleic acids of this kind are suitable as nonradioactive gene probes for detection of complementary nucleotide sequences by hybridization, for example in Northern or Southern blots (disclosed in the European patent specification EP 0 324 474 A1).

25

Digoxigenin group-labeled proteins or glycoproteins are particularly useful for determining, for example, relevant antigens or antibodies directed there against in immunochemical assay methods such as ELISA (enzyme-  
30 linked immunosorbent assay). The biomolecule conjugated with the digoxigenin group is actually detected using an anti-digoxigenin antibody, normally in the form of a conjugate of the Fab fragment of said antibody with a suitable enzyme, such as, for example, alkaline  
35 phosphatase or horseradish peroxidase, as label. The enzymatic activity then serves for quantification via catalysis of a chromogenic, fluorogenic or chemiluminescent reaction. Various antibodies against the digoxigenin group are known (Mudgett-Hunter et al.,

J. Immunol. 129 (1982), 1165-1172; Jeffrey et al., J. Mol. Biol. 248 (1995), 344-360).

The use of antibodies, however, has several  
5 disadvantages. Hence, the preparation of monoclonal  
antibodies in hybridoma cell cultures is complicated,  
and the proteolysis for the Fab fragment and also the  
production of conjugates with reporter enzymes requires  
10 additional difficult processing steps. But even the  
production of antibodies by genetic engineering is not  
simple, and the main reason for this is that antibodies  
as well as their antigen-binding fragments are composed  
of two different polypeptide chains in a structurally  
15 complicated manner. For the genetic manipulation of  
antibodies it is therefore necessary to handle two  
genes simultaneously. Moreover, the yield of correctly  
folded antibody fragments produced by genetic  
engineering is often low. As is known to the skilled  
20 worker, this is even more so when recombinant fusion  
proteins are to be prepared from Fab fragments of  
antibodies and enzymes.

It was therefore the object of the invention to develop  
alternative polypeptide reagents for detection of the  
25 digoxigenin group, which can be produced in a simple  
manner.

In an evolutionary research approach, it has  
surprisingly been found now that muteins of the bilin-  
30 binding protein, which is structurally based on a  
single polypeptide chain (Schmidt and Skerra, Eur. J.  
Biochem. 219 (1994), 855-863), are suitable for  
detecting the digoxigenin group by binding with high  
affinity, whereby the recognition of digoxigenin is  
35 astoundingly selective compared with other steroids.

The present invention thus relates to a polypeptide,  
selected from muteins of the bilin-binding protein,  
which is characterized in that it

(a) is able to bind digoxigenin or digoxigenin conjugates,

(b) does not bind ouabain, testosterone, and 4-aminofluorescein and

5 (c) has an amino acid substitution at at least one of the sequence positions 28, 31, 34, 35, 36, 37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125, and 127 of the bilin-binding protein.

10 In this connection, preference is given to digoxigenin-binding muteins which have an amino acid substitution at at least 4 to 7 or, preferably, at least 8 to 12 of the sequence positions defined above. A particularly preferred mutein is the polypeptide which has the amino  
15 acid sequence depicted as SEQ ID NO. 15.

Outside the region of the amino acid positions 28, 31, 34, 35, 36, 37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125, and 127 the muteins of the present invention may  
20 correspond to the amino acid sequence of the bilin-binding protein from *Pieris brassicae*. On the other hand, the amino acid sequence of the polypeptides of the invention may also have differences to the bilin-binding protein apart from said positions. Bilin-  
25 binding protein sequence variants of this kind comprise naturally occurring and also artificially generated variants, and the deviations mean substitutions, insertions, deletions of amino acid residues and also N- and/or C-terminal additions.

30 For example, the inventive muteins of the bilin-binding protein may have amino acid substitutions which prevent oligomerization of the bilin-binding protein, such as the Asn(1)->Asp substitution, or suppress proteolytic  
35 cleavage within the polypeptide chain, which may occur during production in *E. coli*, such as, for example, by the Lys(87)->Ser substitution. Furthermore, the mutations Asn(21)->Gln and Lys(135)->Met may be introduced into the nucleic acid coding for the muteins

10

20

25

35

- 6 -

35, 36, 37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125, and 127 and subsequent simple or, preferably, repeated selection of muteins with affinity for the digoxigenin group from this library, preferably using free digoxigenin or digitoxigenin for competitive enrichment, provides muteins of the bilin-binding protein which recognize the digoxigenin group, but the affinity is still comparatively low. Renewed mutagenesis of such a mutein at at least one, preferably at at least 3 or 4, or at all of amino acid positions 28, 31, 34, 35, 36 and 37, now followed by a simple or, preferably, repeated enrichment by formation of a complex with the digoxigenin group and by subsequent dissociation of the formed complex in an acidic or basic milieu, then results in obtaining muteins having substantially higher affinity for the digoxigenin group. The digoxigenin group is preferably present as a digoxigenin/biotin double conjugate during said enrichment.

Surprisingly, it has now been found that the affinity constant between such polypeptides of the invention and digoxigenin is at least  $10^7 \text{ M}^{-1}$ . This means in other words that the dissociation constant of the complex between the polypeptide of the invention and digoxigenin is 100 nM or less. Individual species even show dissociation constants of 35 nM or less, as illustrated in the Examples.

Besides digoxigenin, the inventive muteins of the bilin-binding protein can also bind digoxigenin derivatives as ligands, for example digoxin, digitoxin or digitoxigenin. Furthermore, the inventive muteins of the bilin-binding protein may bind conjugates of said chemical compounds, i.e. nucleic acids, polypeptides, carbohydrates, other natural or synthetic biomolecules, macromolecules or low molecular weight compounds which are covalently linked or linked via a metal complex to digoxigenin, digoxin, digitoxin or digitoxigenin.

Preference is given to using for the preparation of such conjugates the reactive derivatives of digoxigenin, digoxin, digitoxin or digitoxigenin, which are known to the skilled worker and are stated, for example, further above.

Preferred muteins of the invention, which were obtained by the two-stage process described, show, compared with the affinity for digoxigenin, an even higher affinity for digitoxin or digitoxigenin, whose steroid system differs from that of digoxigenin only by the absence of a hydroxyl group. Surprisingly, these muteins show distinctive specificity with respect to the digoxigenin or digitoxigenin group, and this is shown by the fact that other steroids or steroid groups such as ouabain or testosterone are bound with much less affinity, if at all. Fluorescein derivatives such as 4-amino-fluorescein, too, are evidently not bound. This means that ouabain, testosterone or 4-aminofluorescein in each case exhibit a dissociation constant of at least 10  $\mu$ M, preferably at least 100  $\mu$ M, with respect to the inventive muteins of the bilin-binding protein.

This property of specificity distinguishes said muteins considerably from other muteins of the bilin-binding protein and also from antibodies directed against the digoxigenin group, such as, for example, the antibody 26-10 (Chen et al., Protein Eng. 12 (1999), 349-356), which binds ouabain with substantial affinity, and gives the inventive muteins of the bilin-binding protein a particular advantage. It is surprising that particularly the additional amino acid substitutions at positions 28, 31, 34, 35, 36, and 37 lead to the preferred muteins of the bilin-binding protein. Preference is therefore given to those muteins which carry at least one, preferably at least 3 or 4, or all of the amino acid substitutions Glu(28)->Gln, Lys(31)->Ala, Asn(34)->Asp, Ser(35)->His, Val(36)->Ile and Glu(37)->Thr.



Particularly preferred muteins of the invention carry, when compared to the bilin-binding protein, at least one, at least 4 to 7, or, preferably, at least 8 to 12  
 5 of the amino acid substitutions selected from Glu(28)->Gln, Lys(31)->Ala, Asn(34)->Asp, Ser(35)->His, Val(36)->Ile, Glu(37)->Thr, Asn(58)->Arg, His(60)->Ser, Ile(69)->Ser, Leu(88)->Tyr, Tyr(90)->Ile, Lys(95)->Gln, Asn(97)->Gly, Tyr(114)->Phe, Lys(116)->Ser, Gln(125)-  
 10 >Met and Phe(127)->Leu. The representation chosen indicates in each case first the amino acid in the natural bilin-binding protein (SWISS-PROT database accession code P09464) together with the sequence position for the mature polypeptide in brackets, and  
 15 the corresponding amino acid in a mutein of the invention is stated after the arrow. Very particularly preferred muteins according to this invention carry all of the amino acid substitutions mentioned.

20 Surprisingly, position 93 of the bilin-binding protein is unchanged in the muteins of the invention, although this amino acid, too, had been affected by the mutagenesis for preparing the random library. Preferred muteins of the bilin-binding protein therefore carry  
 25 the amino acid Val at said position.

It is an advantage for particular detection methods to use the muteins of the bilin-binding protein of the present invention in a labeled form. Accordingly, this  
 30 invention further relates to a polypeptide of the invention which is characterized in that it carries at least one label. Suitable labeling groups are known to the skilled worker and include enzyme label, radioactive label, fluorescent label, chromophoric  
 35 label, (bio)luminescent label or a label containing haptens, biotin, metal complexes, metals or colloidal gold. Very generally, labeling is possible with substances or enzymes which generate a determinable substance in a chemical or enzymatic reaction. In this

connection it is possible to couple all known labels for antibodies to the muteins of the invention, too.

5 A possibility which is particularly advantageous for practical application is to use the inventive muteins of the bilin-binding protein in the form of fusion proteins. Techniques for preparing such fusion proteins by means of genetic engineering methods are known to the skilled worker. Suitable fusion partners for the  
10 muteins of the invention would be enzymes and other polypeptides, proteins or protein domains. Such fusions would be suitable for providing the mutein of the bilin-binding protein with additional properties such as, for example, enzymatic activity or affinity for  
15 other molecules, such as proteins, macromolecules or low molecular weight ligands.

For example, fusions are possible with enzymes which catalyze chromogenic or fluorogenic reactions or may  
20 serve for the release of cytotoxic agents. Further examples for fusion partners which may be advantageous in practice are binding domains such as the albumin-binding domain or the immunoglobulin-binding domain of protein G or protein A, antibody fragments,  
25 oligomerization domains, toxins or other binding proteins and functional parts thereof and also affinity peptides such as, for example, the Strep-tag or the Strep-tag II (Schmidt et al., J. Mol. Biol. 255 (1996), 753-766). Suitable fusion partners are also proteins  
30 having particular chromogenic or fluorogenic properties, such as, for example, green fluorescent protein. Another suitable fusion partner would be the coat protein III of a filamentous bacteriophage, such as M13, f1 or fd, or a fragment of said coat protein.

35

Very generally, the term fusion protein is intended here to mean also those inventive muteins of the bilin-binding protein, which are equipped with a signal sequence. Signal sequences at the N-terminus of the

polypeptide of the invention may serve for the purpose of directing said polypeptide during biosynthesis into a particular cell compartment, for example the *E. coli* periplasm or the lumen of the endoplasmic reticulum of a eukaryotic cell, or into the medium surrounding the cell. The signal sequence is typically cleaved off by a signal peptidase. In addition, it is also possible to use other signal or targeting sequences which need not necessarily be located at the N-terminus of the polypeptide and which make it possible to locate said polypeptide in specific cell compartments. A preferred signal sequence for secretion into the *E. coli* periplasm is the OmpA signal sequence. A large number of further signal sequences and also targeting sequences are known in the prior art.

An advantage of the inventive muteins of the bilin-binding protein is the suitability of both their N-terminus and their C-terminus for preparing fusion proteins. In contrast to antibodies, in which the N-terminus of both the light and the heavy immunoglobulin chain are in spatial proximity to the antigen binding site, it is possible to use in the polypeptides of the invention both ends of the polypeptide chain for the preparation of fusion proteins, without adversely affecting ligand binding.

The invention therefore also relates to fusion proteins of muteins of the bilin-binding protein in which an enzyme, another protein or a protein domain, a signal sequence and/or an affinity peptide is fused to the amino terminus of the polypeptide in an operable manner. The invention yet further relates to fusion proteins of bilin-binding protein muteins or of fusion proteins with the amino terminus of bilin-binding protein muteins in which an enzyme, another protein or a protein domain, a targeting sequence and/or an affinity peptide is fused to the carboxy terminus of the polypeptide in an operable manner.

A preferred enzyme for constructing the fusion proteins of the invention is bacterial alkaline phosphatase (Sowadski et al., J. Mol. Biol. 186 (1985) 417-433),  
5 which may be attached either at the N-terminus or at the C-terminus of a mutein of the bilin-binding protein. In addition, such a fusion protein may carry a signal sequence such as, for example, OmpA or PhoA, which effects secretion of said fusion protein into the  
10 *E. coli* periplasm, where the disulfide bonds of the polypeptide chain may form efficiently. Furthermore, it may be equipped with an affinity peptide such as, for example, the Strep-tag II, which allows easy purification of said fusion protein. Specific fusion  
15 proteins of the invention are described in the Examples. An advantage of a fusion protein of this kind is its ability to catalyze directly a chromogenic, fluorogenic or chemiluminescent detection reaction, which simplifies its use for detection of the  
20 digoxigenin group.

Another advantage of using alkaline phosphatase for constructing fusion proteins of the invention is the fact that this enzyme forms a stable homodimer and,  
25 consequently, confers the property of bivalence on the bilin-binding protein mutein as part of the fusion protein. In this way, binding of the digoxigenin group may result in an avidity effect, which increases detection sensitivity. Such an avidity effect can be  
30 expected in particular if the digoxigenin-labeled molecule is adsorbed to a solid phase, is present in oligomeric or membrane-bound form or is conjugated with a plurality of digoxigenin groups. Analogously, other homodimeric enzymes are suitable for preparing bivalent  
35 fusion proteins containing the inventive muteins of the bilin-binding protein.

Apart from bacterial alkaline phosphatase, it is also possible to use phosphatases from eukaryotic organisms,

such as, for example, calf intestine phosphatase (CIP), for preparing fusion proteins of the invention. Said phosphatases are frequently distinguished by higher enzymatic activity (Murphy and Kantrowitz, Mol. Microbiol. 12 (1994), 351-357), which may result in higher detection sensitivity. It is also possible to use mutants of bacterial alkaline phosphatase, which have improved catalytic activity (Mandecki et al., Protein Eng. 4 (1991), 801-804), for constructing fusion proteins of the invention. Other enzymes known to the skilled worker which catalyze chromogenic, fluorogenic or chemiluminescent reactions, such as, for example,  $\beta$ -galactosidase or horseradish peroxidase, are also suitable for preparing fusion proteins of the invention. Moreover, all these enzymes may likewise be employed for labeling muteins of the bilin-binding protein by conjugating them, for example by using common coupling reagents, with the separately obtained mutein or a fusion protein of the mutein.

In another aspect, the present invention relates to a nucleic acid which comprises a sequence coding for a mutein or a fusion protein of a mutein of the bilin-binding protein. This nucleic acid may be part of a vector on which an operatively functional environment for expressing the nucleic acid is present. A large number of suitable vectors is known from the prior art and is not described in detail here. An operatively functional environment means those elements which allow, assist, facilitate and/or increase transcription and/or subsequent processing of an mRNA. Examples of elements of this kind include promoters, enhancers, transcription initiation sites, and transcription termination sites, translation initiation sites, polyadenylation signals, etc. In a preferred embodiment, such nucleic acids of the invention comprise a nucleic acid sequence which encodes the polypeptide sequence depicted as SEQ ID NO:15. Owing to the degeneracy of the genetic code, it is clear to the

- 13 -

skilled worker that the nucleotide sequence stated as SEQ ID NO:15 represents only a single nucleotide sequence from the group of nucleotide sequences encoding the polypeptide according to SEQ ID NO:15.

5

The nucleic acid of the invention or its environment may be designed such that biosynthesis of the polypeptide takes place in the cytosol, in which case the polypeptide sequence being preceded, where appropriate, by a start methionine. In a preferred embodiment, however, an N-terminal signal sequence is used, in particular the OmpA or PhoA signal sequence, in order to direct the polypeptide of the invention into the *E. coli* periplasm, where the signal sequence is cleaved off by the signal peptidase and the polypeptide chain is able to fold with oxidative formation of the disulfide bonds. Eukaryotic signal sequences may be used in order to secrete the polypeptide of the invention in a eukaryotic host organism.

15  
20

In principle, both prokaryotic, preferably *E. coli*, and eukaryotic cells such as, for example, yeasts are considered for expression of the nucleic acid of the invention.

25

In yet another aspect, the present invention relates to a method for preparing an inventive mutein or fusion protein of a mutein of the bilin-binding protein, which method is characterized in that the nucleic acid coding for the mutein or the fusion protein of a mutein of the bilin-binding protein is expressed in a bacterial or eukaryotic host cell and the polypeptide is obtained from the cell or the culture supernatant. For this purpose, normally a suitable host cell is first transformed with a vector which comprises a nucleic acid coding for a polypeptide of the invention. The host cell is then cultured under conditions under which

30  
35

bio-synthesis of the polypeptide occurs, and the polypeptide of the invention is obtained.

With respect to the preparation method, it must be  
5 taken into account that the inventive muteins of the  
bilin-binding protein have two structural disulfide  
bonds and that additional disulfide bonds may be  
present in corresponding fusion proteins. The formation  
of said disulfide bonds, which takes place during  
10 protein folding, is normally ensured if the polypeptide  
of the invention is directed with the aid of a suitable  
signal sequence into a cell compartment containing an  
oxidizing thiol/disulfide redox milieu, for example  
into the bacterial periplasm or the lumen of the  
15 endoplasmic reticulum of a eukaryotic cell. In this  
respect, the polypeptide of the invention can be  
liberated by cell fractionation or obtained from the  
culture supernatant. It is possible, where appropriate,  
to increase the folding efficiency by overproducing  
20 protein disulfide isomerases, for example *E. coli* DsbC  
protein, or proteins that assist folding.

On the other hand, it is possible to produce a  
polypeptide of the invention in the cytosol of a host  
25 cell, preferably *E. coli*. The said polypeptide may then  
be obtained, for example, in the form of inclusion  
bodies and afterwards be renatured *in vitro*. Depending  
on the intended use, the protein can be purified by  
means of various methods known to the skilled worker. A  
30 suitable method for purifying the inventive muteins of  
the bilin-binding protein is, for example, affinity  
chromatography using a column material which carries  
digoxigenin groups. In order to purify fusion proteins  
of the muteins of the bilin-binding protein, it is  
35 possible to utilize the affinity properties of the  
fusion protein, which are known from the prior art, for  
example those of the Strep-tag or the Strep-tag II  
(Schmidt and Skerra, J. Chromatogr. A 676 (1994), 337-  
345; Voss and Skerra, Protein Eng. 10 (1997), 975-982),

those of the albumin binding domain (Nygren et al., J. Mol. Recogn. 1 (1988), 69-74) or those of alkaline phosphatase (McCafferty et al., Protein Eng. 4 (1991) 955-961). The fact that the muteins of the bilin-binding protein consist only of a single polypeptide chain is advantageous for the methods for preparing the polypeptides of the invention, since no care needs to be taken either of synthesizing several different polypeptide chains within a cell simultaneously or of different polypeptide chains associating with one another in a functional manner.

The possibilities for practical application of the inventive muteins of the bilin-binding protein essentially correspond to those for conventional antibodies or antibody fragments with binding affinity for digoxigenin. Accordingly, the invention also relates to the use of a mutein of the invention or of a fusion protein of a mutein of the bilin-binding protein in a method for detecting, determining, immobilizing or removing digoxigenin or conjugates of digoxigenin with proteins, nucleic acids, carbohydrates, other biological or synthetic macromolecules or low molecular weight chemical compounds.

The inventive muteins of the bilin-binding protein or their fusion proteins can be used in detection methods essentially in a manner analogous to corresponding detection methods known for anti-digoxigenin antibodies and also fragments and/or conjugates thereof. In a further aspect, the present invention therefore relates to a method for detecting the digoxigenin group, in which method a mutein of the bilin-binding protein or a fusion protein of a mutein of the bilin-binding protein is brought into contact with digoxigenin or with digoxigenin conjugates under conditions suitable for effecting binding of the mutein to the digoxigenin group and the mutein or the fusion protein of the mutein is determined.



For this purpose, the mutein may be labeled directly, for example by covalent coupling. It is, however, also possible to use indirect labeling, for example by means  
5 of labeled antibodies against the bilin-binding protein or muteins thereof or against domains of fusion proteins of these muteins. The use of inventive fusion proteins containing an enzyme, for example alkaline phosphatase, instead of a labeled mutein of the bilin-  
10 binding protein is particularly advantageous. In this case, it is possible to design the determination method with a particularly small number of process steps, whereby, for example, the ability of the enzyme as part  
15 of the fusion protein to catalyze a chromogenic, fluorogenic or luminescent detection reaction may be directly utilized. Here, the fact that such fusion proteins are readily available is a particular advantage compared with corresponding fusion proteins  
20 of conventional antibodies. Utilization of the above-described avidity effect in the case of an oligomeric fusion protein is a further advantage in such a method.

It is possible to carry out a method for determining the digoxigenin group, for example, for qualitatively  
25 detecting nucleic acids conjugated with the digoxigenin group in Southern or Northern blots or proteins conjugated with the digoxigenin group in Western blots. A determination method may also be carried out quantitatively for detecting proteins conjugated with  
30 the digoxigenin group in an ELISA. In addition, a determination method of the invention is also suitable for indirect detection of proteins not conjugated with digoxigenin or of other molecules by using a binding protein which is directed against the protein or  
35 molecule, for example an antibody or its fragment, and which is conjugated with the digoxigenin group. Indirect detection of the nucleic acids not conjugated with digoxigenin is also possible by using a gene probe which hybridizes with said nucleic acid and which is

conjugated with the digoxigenin group. An application in medical diagnostics or therapy results furthermore from the determination of digoxigenin, digoxin, digitoxin or digitoxigenin, without these ligands  
5 having to be conjugated with another molecule.

The muteins of the invention or fusion proteins thereof may also be used for immobilizing a molecule conjugated with the digoxigenin group. This immobilization is  
10 preferably carried out on solid phases coated with the muteins or their fusion proteins, such as, for example, microtiter plates, immunosticks, microbeads made of organic, inorganic or paramagnetic materials, or sensor surfaces.

15 Correspondingly, it is likewise possible to use the muteins of the invention or fusion proteins thereof for removing digoxigenin, digoxin, digitoxin or digitoxigenin, or a molecule conjugated with one of  
20 these compounds. In this case, in addition to the solid phases mentioned, column materials are also considered for coating with the muteins or their fusion proteins. Preferably, said coating is carried out on suitable column materials by coupling by means of chemically  
25 reactive groups. Column materials coated in this way may be used for removing from a solution substances conjugated with digoxigenin groups and also, where appropriate, complexes of such substances with other molecules.

30 Thus, it is possible, for example, to remove antigens from a solution by adding to the solution antibodies which are directed against the antigens and are conjugated with the digoxigenin group, and contacting  
35 the resulting solution with said column material under conditions under which complex formation between the digoxigenin groups and an inventive mutein of the bilin-binding protein or its fusion protein occurs. Following such a removal, it is also possible, where

appropriate, to elute the substance conjugated with the digoxigenin. This elution may be carried out by competition with digoxin, digoxigenin, digitoxin or digitoxigenin and also, for example, by lowering or increasing the pH of the solution. In a competitive elution it is possible to utilize in an advantageous manner the higher binding affinity of the muteins of the invention for digitoxigenin or digitoxin compared with the digoxigenin group. In this way it is possible to isolate or purify a substance conjugated with digoxigenin.

The invention is further illustrated by the following Examples and attached drawings, in which:

Figure 1 represents in each case a fluorescence titration of the Strep-tag II-fused mutein DigA16 with the ligands digoxigenin, digitoxigenin, and ouabain;

Figure 2 depicts diagrammatically the expression vectors pBBP27 (A) and pBBP29 (B) for preparing fusion proteins of mutein DigA16 with alkaline phosphatase;

Figure 3 demonstrates quantitative detection of biomolecules conjugated with digoxigenin groups by fusion proteins of mutein DigA16 with alkaline phosphatase in an ELISA;

Figure 4 shows qualitative detection of biomolecules conjugated with digoxigenin groups by fusion proteins of mutein DigA16 with alkaline phosphatase on a Western blot.

Figure 1 shows the graphic representation of results from Example 3 in which different concentrations of the steroids digoxigenin (squares), digitoxigenin (circles) and ouabain (rhomboids) were added to a 1  $\mu$ M solution

of mutein DigA16. The particular protein fluorescence intensities were measured at an excitation wavelength of 295 nm and an emission wavelength of 345 nm and plotted as a function of the actual total steroid  
5 concentration in the particular reaction mixture. Finally, the data points were fitted to a regression curve by means of non-linear regression.

Figure 2 shows a drawing of the expression vectors  
10 pBBP27 (A) and pBBP29 (B). pBBP27 codes for a fusion protein of bacterial alkaline phosphatase with its own signal sequence, a peptide linker having the sequence Pro-Pro-Ser-Ala, the mutein DigA16 and also the Strep-tag II affinity tag. The corresponding structural gene  
15 is followed by the *dsbC* structural gene (including its ribosomal binding site) from *E. coli* (Zapun et al., Biochemistry 34 (1995), 5075-5089) as second cistron. The artificial operon formed in this way is under joint transcriptional control of the tetracycline  
20 promoter/operator ( $tet^{P/O}$ ) and ends at the lipoprotein transcription terminator ( $t_{1pp}$ ). Further vector elements are the origin of replication (*ori*), the intergenic region of filamentous bacteriophage f1 (*f1-IG*), the ampicillin resistance gene (*bla*) coding for  $\beta$ -lactamase  
25 and the tetracycline repressor gene (*tetR*). pBBP29 codes for a fusion protein of the OmpA signal sequence, the mutein DigA16, the Strep-tag II affinity tag, a peptide linker consisting of five glycine residues, and bacterial alkaline phosphatase without its N-terminal  
30 amino acid arginine. The vector elements outside this region are identical to vector pBBP27.

Figure 3 shows a graphic representation of the data from Example 4 in which digoxigenin groups were  
35 detected quantitatively with the aid of mutein DigA16 fusion proteins as gene products of vectors pBBP27 (closed symbols) and pBBP29 (open symbols). Here, the digoxigenin groups were coupled on the one hand to bovine serum albumin (BSA, squares) or, on the other

hand, to chicken egg albumin (ovalbumin, triangles). The control data shown are those obtained when using underivatized bovine serum albumin and the fusion protein encoded by pBBP27 (open circles). The enzymatic activity corresponding to the particular bound fusion protein was monitored spectrophotometrically at 405 nm on the basis of p-nitrophenyl phosphate hydrolysis. Curve fitting was carried out by non-linear regression with the aid of the Kaleidagraph computer program (Abelbeck Software) by means of the equation

$$[P \cdot L] = [L]_t [P]_t / (K_d + [P]_t).$$

Here,  $[P]_t$  corresponds to the total fusion protein concentration used in the particular microtiter plate well.  $[P \cdot L]$  is determined on the basis of the enzymatic activity of alkaline phosphatase. The total concentration of digoxigenin groups  $[L]_t$ , constant within a concentration series, per well and the dissociation constant  $K_d$  were fitted as parameters by non-linear regression.

Figure 4 shows the result of a Western blot experiment from Example 4 for qualitative detection of biomolecules conjugated with digoxigenin groups by means of the mutein DigA16 fusion proteins encoded by pBBP27 (lanes 1 and 2) and pBBP29 (lanes 3 and 4). For comparison, a 15% strength SDS polyacrylamide gel of the biomolecules, stained with Coomassie Brilliant Blue, is also shown (lanes 5 and 6). Here, a mixture of 0.5  $\mu$ g of underivatized BSA, underivatized ovalbumin and underivatized RNaseA was fractionated in each case in lanes 1, 3 and 5. A mixture of 0.5  $\mu$ g of BSA coupled to digoxigenin groups, ovalbumin coupled to digoxigenin groups and RNaseA coupled to digoxigenin groups was fractionated in each case in lanes 2, 4 and 6.

#### Examples

Unless stated otherwise, the genetic engineering methods familiar to the skilled worker, as described, for example, in Sambrook et al. (Molecular Cloning. A Laboratory Manual (1989), Cold Spring Harbor Press) were used.

10 Example 1: Preparation of a library for muteins of the bilin-binding protein, phagemid presentation and selection of a mutein with binding affinity for digoxigenin

A library for muteins of the bilin-binding protein was prepared by subjecting the amino acid sequence positions 34, 35, 36, 37, 58, 60, 69, 88, 90, 93, 95, 15 97, 114, 116, 125 and 127 of the bilin-binding protein to a concerted mutagenesis in multiple steps by means of the polymerase chain reaction (PCR). The PCR reactions were initially carried out in two separate amplification steps in a volume of in each case 50 µl, 20 and 10 ng of pBBP20 phasmid DNA (SEQ ID NO:1) as template using in each case 25 pmol of two primers (SEQ ID NO:2 and SEQ ID NO:3 in one mixture and SEQ ID NO:4 and SEQ ID NO:5 in a second mixture) which had been synthesized according to the generally known 25 phosphoramidite method were used.

Furthermore, the reaction mixture contained 5 µl of 10xTaq buffer (100 mM Tris/HCl pH 9.0, 500 mM KCl, 1% v/v Triton X-100), 3 µl of 25 mM MgCl<sub>2</sub> and 4 µl of dNTP 30 mix (2.5 mM dATP, dCTP, dGTP, dTTP). After filling up with water, the mixture was overlaid with mineral oil and heated to 94°C in a programmable thermostating block for 2 min. Then 2.5 u of *Taq* DNA polymerase (5 u/µl, Promega) were added and 20 temperature cycles 35 of 1 min at 94°C, 1 min at 60°C and 1.5 min at 72°C were carried out, followed by an incubation at 60°C for 5 min. The desired amplification products were isolated via preparative agarose gel electrophoresis from low melting point agarose (Gibco BRL), using the Jetsorb

DNA extraction kit (Genomed) according to the manufacturer's instructions.

A relevant section of the pBBP20 nucleic acid sequence is shown together with the encoded amino acid sequence as SEQ ID NO:1 in the sequence listing. The section starts with a hexanucleotide sequence which was obtained by ligating an *Xba*I overhang with an *Spe*I overhang complementary thereto and ends with the *Hind*III cleavage site. The vector elements outside this region are identical to vector pASK75 whose complete nucleotide sequence is stated in the German Offenlegungsschrift DE 44 17 598 A1.

The subsequent amplification step was carried out in a 100 µl mixture, and in each case approx. 6 ng of the two isolated fragments as template using 50 pmol of each of the two primers SEQ ID NO:6 and SEQ ID NO:7 and also 1 pmol of oligodeoxynucleotide SEQ ID NO:8. The remaining components of the PCR mixture were added in twice the amount, as in the preceding amplification steps. The PCR was carried out in 20 temperature cycles of 1 min at 94°C, 1 min at 55°C, and 1.5 min at 72°C, followed by a final incubation at 60°C for 5 min. The fragment obtained was again isolated by preparative agarose gel electrophoresis.

For cloning this fragment which represented the mutein library in the form of a mixture of nucleic acids it was first cut with the restriction enzyme *Bst*XI (New England Biolabs) according to the manufacturer's instructions. The nucleic acid fragment obtained (335 base pairs, bp) was purified again by means of preparative agarose gel electrophoresis. Analogously, pBBP20 vector DNA was cut with *Bst*XI and the larger of the two fragments (3971 bp) was isolated.

For ligation, 0.93 µg (4.2 pmol) of the PCR fragment and 11 µg (4.2 pmol) of the vector fragment were

incubated in the presence of 102 Weiss units of T4 DNA ligase (New England Biolabs) in a total volume of 500  $\mu$ l (50 mM Tris/HCl pH 7.8, 10 mM MgCl<sub>2</sub>, 10 mM DTT, 1 mM ATP, 50  $\mu$ g/ml BSA) at 16°C for two days. The DNA  
5 was then precipitated by adding 10  $\mu$ g of yeast tRNA (Boehringer Mannheim), 25  $\mu$ l of 5 M ammonium acetate and 100  $\mu$ l of ethanol to in each case 24  $\mu$ l of the ligation mixture. Incubation at -20°C for 3 days was followed by centrifugation (25 min, 16000 g, 4°C). The  
10 precipitate was washed in each case with 200  $\mu$ l of ethanol (70% v/v, -20°C) and dried under vacuum. Finally, the DNA was taken up in 43.6  $\mu$ l of TE/10 (1 mM Tris/HCl pH 8.0, 0.1 mM EDTA). The DNA concentration of the solution obtained was estimated by analytical  
15 agarose gel electrophoresis on the basis of the fluorescence intensity of the bands stained with ethidium bromide in comparison with a DNA size standard of known concentration.

20 Preparation of electrocompetent cells of the *E. coli* K12 strain XL1-Blue (Bullock et al., BioTechniques 5 (1987), 376-379) was carried out according to the methods described by Tung and Chow (Trends Genet. 11 (1995), 128-129) and by Hengen (Trends Biochem. Sci. 21  
25 (1996), 75-76). 1 l of LB medium was adjusted to an optical density at 600 nm, OD<sub>600</sub> = 0.08 by adding a stationary XL1-Blue overnight culture and incubated in a 3 l Erlenmeyer flask at 200 rpm and 26°C. After reaching OD<sub>600</sub> = 0.6, the culture was cooled on ice for  
30 30 min and then centrifuged at 4000 g and 4°C for 15 min. The cell sediment was washed twice with in each case 500 ml of ice cold 10% w/v glycerol and finally resuspended in 2 ml of ice cold GYT medium (10% w/v glycerol, 0.125% w/v yeast extract, 0.25% w/v  
35 tryptone).

Electroporation was carried out by using the Easyjec T Basic system (EquiBio) with the corresponding cuvettes (electrode distance 2 mm). All operational steps were



carried out in a cold room at 4°C. 5 to 6 µl of the above-described DNA solution (245 ng/µl) were in each case mixed with 40 µl of the cell suspension, incubated on ice for 1 min and then transferred into the cuvette.

5 After electroporation, the suspension was immediately diluted in 2 ml of fresh ice-cold SOC medium (2% w/v tryptone, 0.5% w/v yeast extract, 10 mM NaCl, 10 mM MgSO<sub>4</sub>, 10 mM MgCl<sub>2</sub>) and agitated at 37°C and 200 rpm for 60 min. The cells were then sedimented at 3600 g for in

10 each case 2 min, resuspended in 1 ml of LB medium containing 100 µg/ml of ampicillin (LB/Amp) and plated out at 200 µl each on agar plates (140 mm in diameter) with LB/Amp medium. Using a total of 10.7 µg of the ligated DNA in eight electroporation mixtures produced

15 in this way  $3.73 \cdot 10^8$  transformants which were distributed on 40 agar plates.

After incubation at 32°C for 14 h, the colonies obtained in this way were scraped off the agar plates

20 with the addition of in each case 10 ml of 2xYT/Amp medium, transferred to a sterile Erlenmeyer flask and agitated at 37°C, 200 rpm for 20 min to complete resuspension. 50 ml of 2xYT/Amp medium prewarmed to 37°C were inoculated with 2.88 ml of said suspension so

25 that the cell density was 1.0 OD<sub>550</sub>. This culture was incubated at 37°C, 160 rpm for 6 h to reach a stationary cell density, and phasmid DNA was isolated with the aid of the plasmid Midi kit (Qiagen) according to the manufacturer's instructions. Finally, the DNA

30 was taken up in 100 µl of TE (10 mM Tris/HCl pH 8.0, 1 mM EDTA) and stored at 4°C for further use.

In order to prepare a library of recombinant phagemids (Kay et al., Phage Display of Peptides and Proteins - A

35 Laboratory Manual (1996), Academic Press) which carry the muteins of the bilin-binding protein as a fusion with the truncated coat protein pIII, the phasmid DNA obtained in this way was used for transformation of electrocompetent cells of *E. coli* XL1-Blue.

Electroporation was carried out as described above with the aid of the Easyjec T Basic system. In a total of 13 mixtures, 40  $\mu$ l of the cell suspension of electrocompetent cells were in each case transformed with in each case 2  $\mu$ g of the DNA in a volume of 5  $\mu$ l. After electroporation, the cell suspension obtained from each mixture was diluted immediately in 2 ml of fresh ice-cold SOC medium and agitated at 37°C and 200 rpm for 60 min.

10

The mixtures were combined (volume = 26 ml) and 74 ml of 2xYT medium and 100  $\mu$ l of ampicillin (stock solution 100 mg/ml, final concentration 100 mg/l) were added. The total number of transformants obtained was estimated at  $1.1 \cdot 10^{10}$  by plating out 100  $\mu$ l of a  $1:10^5$  dilution of the obtained suspension on agar plates containing LB/Amp medium. After incubation at 37°C and 160 rpm for 60 min, the culture was infected with 500  $\mu$ l of VCS-M13 helper phage ( $1.1 \cdot 10^{12}$  pfu/ml, Stratagene) and agitated at 37°C, 160 rpm for a further 60 min. Subsequently, 200  $\mu$ l of kanamycin (stock solution 35 mg/ml, final concentration 70 mg/l) were added, the incubator temperature was lowered to 26°C and, after 10 min, anhydrotetracycline (50  $\mu$ l of a 50  $\mu$ g/ml stock solution in dimethylformamide, final concentration 25  $\mu$ g/l) was added to induce gene expression. Finally, for production of the phagemids the culture was incubated at 26°C, 160 rpm for 7 h.

25

30 The cells were removed by centrifugation of the culture (15 min, 12000 g, 4°C). The supernatant containing the phagemid particles was sterile-filtered (0.45  $\mu$ m), mixed with 1/4 volume (25 ml) of 20% w/v PEG 8000, 15% w/v NaCl and incubated at 4°C overnight. After 35 centrifugation (20 min, 18000 g, 4°C), the precipitated phagemid particles were dissolved in a total of 4 ml of cold PBS (4 mM  $\text{KH}_2\text{PO}_4$ , 16 mM  $\text{Na}_2\text{HPO}_4$ , 115 mM NaCl, pH 7.4). The solution was incubated on ice for 30 min and distributed into four 1.5 ml reaction vessels at equal

volumes. After removing undissolved components by centrifugation (5 min, 18500 g, 4°C), the supernatant was transferred in each case to a new reaction vessel.

5 The phagemid particles were again precipitated by mixing with 1/4 volume (in each case 0.25 ml per reaction vessel) of 20% w/v PEG 8000, 15% w/v NaCl and incubating on ice for 60 min. After centrifugation (20 min, 18500 g, 4°C), the supernatant was removed and  
10 the precipitated phagemid particles were each dissolved in 0.5 ml of PBS. After incubation on ice for 30 min, centrifugation (5 min, 18500 g, 4°C) was repeated to clarify the solution. The supernatant containing the phagemid particles (between  $1 \cdot 10^{12}$  and  $5 \cdot 10^{12}$  cfu/ml)  
15 was then used for affinity enrichment.

For affinity enrichment of the recombinant phagemids presenting the muteins of the bilin-binding protein Immuno-Sticks (NUNC) were used. These were coated  
20 overnight with 800 µl of a conjugate (100 µg/ml) of ribonuclease A (RNaseA) and digoxigenin in PBS.

The conjugate was prepared by adding 1.46 µmol (0.96 mg) of digoxigenin-3-O-methylcarbonyl-ε-amino-caproic acid N-hydroxysuccinimide ester (DIG-NHS, Boehringer Mannheim) in 25 µl of DMSO in µl steps and  
25 with constant mixing to 0.73 µmol (10 mg) of RNaseA (Fluka) in 1 ml of 5% w/v sodium hydrogen carbonate. The mixture was incubated with stirring at room  
30 temperature (RT) for 1 h. Excess reagent was then removed from the RNaseA conjugate by means of a PD-10 gel filtration column (Pharmacia) according to the manufacturer's instructions.

35 Unoccupied binding sites on the Immuno-Stick surface were saturated by incubation with 1.2 ml of 2% w/v BSA in PBST (PBS with 0.1% v/v Tween 20) at RT for 2 h. After three short washes with in each case 1.2 ml of PBST, the Immuno-Stick was incubated in a mixture of

250  $\mu$ l of phagemid solution and 500  $\mu$ l of blocking buffer (2% w/v BSA in PBST) at RT for 1 h.

For removing unbound phagemids the solution was  
5 stripped off and the Immuno-Stick was washed eight times with in each case 950  $\mu$ l of PBST for 2 min. Finally, adsorbed phagemids were competitively eluted during a 15 minute incubation of the Immuno-Stick with  
10 950  $\mu$ l of a 2 mM solution of digoxigenin in PBS (for this purpose, 0.742 mg of digoxigenin (Fluka) were dissolved in 19.2  $\mu$ l of DMF and added to 930.8  $\mu$ l of PBS).

The phagemids were propagated by heating 950  $\mu$ l of  
15 solution of the elution fraction obtained (between  $10^6$  and  $10^8$  colony-forming units, depending on the selection cycle) briefly to 37°C, mixing the solution with 4 ml of an exponentially growing culture of *E. coli* XL1-Blue ( $OD_{550} = 0.5$ ) and incubated at 37°C,  
20 200 rpm for 30 min. The phagemid-infected cells were then sedimented (2 min, 4420 g, 4°C), resuspended in 800  $\mu$ l of fresh 2xYT medium and plated out on four agar plates containing LB/Amp medium (140 mm in diameter). After incubation at 32°C for 14 h, the colonies  
25 obtained in this way were scraped off the agar plates with the addition of in each case 10 ml of 2xYT/Amp medium, transferred to a sterile Erlenmeyer flask and agitated at 37°C, 200 rpm for 20 min to complete resuspension.

30

For repeated production and affinity enrichment of phagemid particles 50 ml of 2xYT/Amp medium prewarmed to 37°C were inoculated with 0.2 to 1 ml of said suspension so that the cell density was  $OD_{550} = 0.08$ .  
35 This culture was incubated at 37°C, 160 rpm to a cell density of  $OD_{550} = 0.5$ , infected with 250  $\mu$ l of VCS-M13 helper phage ( $1.1 \cdot 10^{12}$  pfu/ml, Stratagene), and the procedure was continued as already described above.

The phagemids obtained from the first affinity concentration were used to carry out a series of eight further enrichment cycles using Immuno-Sticks which had been freshly coated with the digoxigenin-RNaseA conjugate. The phagemids obtained after the last enrichment cycle were again used for infecting *E. coli* XL1-Blue. The mixture of the colonies obtained was scraped off the agar plates using 2xYT/Amp medium and resuspended, as described above. This cell suspension was used to inoculate 50 ml of 2xYT/Amp medium, and the phasmid DNA was isolated using the QIAprep Spin Miniprep kit (QIAGEN) according to the manufacturer's instructions.

In order to be able to produce the muteins of the bilin-binding protein as a fusion protein with the Strep-tag II and the albumin-binding domain, the gene cassette between the two *Bst*XI cleavage sites was subcloned from vector pBBP20 into vector pBBP22. A relevant section of the pBBP22 nucleic acid sequence is represented, together with the encoded amino acid sequence, as SEQ ID NO:9 in the sequence listing. The section starts with the *Xba*I cleavage site and ends with the *Hind*III cleavage site. The vector elements outside this region are identical to vector pASK75.

For this purpose, the DNA isolated from the mixture of the *E. coli* colonies was cut with restriction enzyme *Bst*XI, and the smaller of the two fragments (335 bp) was purified by preparative agarose gel electrophoresis as described above. In the same manner, pBBP22 vector DNA was cut with *Bst*XI and the larger of the two fragments (3545 bp) was isolated.

1.5 Weiss units of T4 DNA ligase (Promega) were added to 50 fmol of each of the two DNA fragments in a total volume of 20  $\mu$ l (30 mM Tris/HCl pH 7.8, 10 mM MgCl<sub>2</sub>, 10 mM DTT, 1 mM ATP) and the mixture was incubated for ligation at 16°C overnight. 5  $\mu$ l of this ligation

mixture were used to transform 200 µl of competent cells of *E. coli* strain TGl-F<sup>-</sup> according to the CaCl<sub>2</sub> method (Sambrook et al., supra), and 2.2 ml of a cell suspension were obtained.

5

The transformants were then screened for production of muteins with binding activity for the digoxigenin group by means of a colony screening assay. For this purpose, a cut-to-fit hydrophilic PVDF membrane (Millipore, type  
10 GVWP, pore size 0.22 µm) marked at one position was placed on an LB/Amp agar plate. 150 µl of the cell suspension from the transformation mixture were plated out evenly on said membrane, and approx. 500 colonies were obtained. The plate was incubated in an incubator  
15 at 37°C for 7.5 h until the colonies were approx. 0.5 mm in diameter.

In the meantime, a hydrophobic membrane (Millipore, Immobilon P, pore size 0.45 µm) which had likewise been  
20 cut to fit was wetted with PBS according to the manufacturer's instructions. Said membrane was then gently agitated in a solution of 10 mg/ml of human serum albumin (HSA, Sigma) in PBS at RT for 4 h. Remaining binding sites on the membrane were saturated  
25 by incubation with 3% w/v BSA, 0.5% v/v Tween 20 in PBS at RT for 2 h. The membrane was washed with 20 ml of PBS for two times for 10 min and then gently agitated in 10 ml of LB/Amp medium to which 200 µg/l of anhydrotetracycline had been added for 10 min. Said  
30 membrane was then marked at one position and placed on a culture plate with LB/Amp agar which additionally contained 200 µg/l of anhydrotetracycline.

The previously obtained hydrophilic membrane on which  
35 colonies had grown was then placed onto the hydrophobic membrane such that the two markings coincided. The culturing plate with the two membranes was incubated at 22°C for 15 h. During this phase, the particular muteins were secreted by the colonies as fusion

proteins and immobilized on the lower membrane by means of complex formation between the albumin-binding domain and the HSA.

5 Subsequently, the upper membrane containing the colonies was transferred to a fresh LB/Amp agar plate and stored at 4°C. The hydrophobic membrane was removed, washed with 20 ml of PBST for three times . 10 min and then incubated in 10 ml of a 10 µg/ml  
10 solution of a conjugate of BSA with digoxigenin in PBST for 1 h.

The conjugate of BSA (Sigma) and digoxigenin was prepared by adding a solution of 3.0 µmol (1.98 mg) of  
15 DIG-NHS in 25 µl of DMSO in µl steps and with constant mixing to 300 nmol (19.88 mg) of BSA (Sigma) in 1.9 ml of 5% w/v sodium hydrogen carbonate. The mixture was incubated with stirring at RT for 1 h and excess reagent was removed from the BSA conjugate by means of  
20 a PD-10 gel filtration column according to the manufacturer's instructions.

In order to detect bound digoxigenin-BSA conjugate, the membrane was incubated, after washing twice in 20 ml of  
25 PBST, with 10 ml of anti-digoxigenin Fab-alkaline phosphatase conjugate (Boehringer Mannheim, diluted 1:1000 in PBST) for 1 h. The membrane was then washed twice with 20 ml PBST and twice with 20 ml of PBST for in each case 5 min and gently agitated in AP buffer  
30 (0.1 M Tris/HCl pH 8.8, 0.1 M NaCl, 5 mM MgCl<sub>2</sub>) for 10 min. For the chromogenic detection reaction, the membrane was incubated in 10 ml of AP buffer to which 30 µl of 5-bromo-4-chloro-3-indolyl phosphate, p-toluidinium salt (BCIP, Roth, 50 µg/ml in  
35 dimethylformamide) and 5 µl of Nitro Blue Tetrazolium (NBT, Sigma, 75 µg/ml in 70% v/v dimethylformamide) had been added, until at the positions of some of the colonies distinct color signals became visible. In this way, digoxigenin-binding activity of the bilin-binding

protein muteins which had been produced in the form of fusion proteins with Strep-tag and ABD by said colonies was detected.

5 Four colonies from the upper membrane, which caused a distinct color signal, were used for preparing cultures in LB/Amp medium of 4 ml in volume. Their plasmid DNA was isolated with the aid of the JETquick Plasmid Miniprep Spin kit (Genomed) according to the  
10 manufacturer's instructions, and the gene section coding for the mutein was subjected to sequence analysis. Sequence analysis was carried out with the aid of the T7 sequencing kit (Pharmacia) according to the manufacturer's instructions by using  
15 oligodeoxynucleotides SEQ ID NO:10 and SEQ ID NO:11. It was found in the process that all four plasmids studied carried the same nucleotide sequence. The corresponding gene product was denoted by DigA (SEQ ID NO:12). The DigA nucleotide sequence was translated into the amino  
20 acid sequence and is represented in the sequence listing.

25 Example 2: Partial random mutagenesis of the DigA mutein and selection of muteins with improved binding affinity for digoxigenin

In order to improve the affinity between the DigA mutein and digoxigenin, which was determined as  $295 \pm 36$  nM according to Example 3, the 6 amino acid  
30 positions 28, 31 and 34-37 in DigA were selected for a more substantial partial random mutagenesis.

For mutating said positions the PCR was carried out using a degenerated oligodeoxynucleotide primer. The  
35 amplification reaction was carried out in a total volume of 100  $\mu$ l, with 2 ng of the vector pBBP22 plasmid DNA coding for DigA (SEQ ID NO:12) being used as template. The reaction mixture contained 50 pmol of the two primers SEQ ID NO:13 and SEQ ID NO:7 and also



the other components according to the method described in Example 1. The PCR was carried out in 20 temperature cycles of 1 min at 94°C, 1 min at 65°C, and 1.5 min at 72°C, followed by a final incubation at 60°C for 5 min.

5 The DNA fragment obtained was isolated by preparative agarose gel electrophoresis and then cut with *Bst*XI according to the manufacturer's instructions. The resulting DNA fragment of 335 bp in length was again purified by preparative agarose gel electrophoresis.

10

The pBBP24 vector DNA was cut with *Bst*XI accordingly and the 4028 bp fragment obtained was isolated. A relevant section of the pBBP24 nucleic acid sequence is represented, together with the encoded amino acid  
15 sequence, as SEQ ID NO:14 in the sequence listing. The section starts with the *Xba*I cleavage site and ends with the *Hind*III cleavage site. The vector elements outside this region are identical to vector pASK75. pBBP24 is virtually identical with pBBP20, wherein the  
20 BBP gene has been inactivated by means of appropriately introduced stop codons.

1.3 µg of the cleaved DNA fragment from the PCR and 16.0 µg of the pBBP24 fragment were incubated for  
25 ligation in the presence of 120 Weiss units of T4 DNA ligase (New England Biolabs) in a total volume of 600 µl (50 mM Tris/HCl pH 7.8, 10 mM MgCl<sub>2</sub>, 10 mM DTT, 1 mM ATP, 50 µg/ml BSA) at 16°C for 18 h. The DNA was then precipitated by adding 10 µg of yeast tRNA  
30 (Boehringer Mannheim), 25 µl of 5 M ammonium acetate and 100 µl of ethanol to in each case 24 µl of the ligation mixture. Incubation at -20°C for two weeks was followed by centrifugation (20 min, 16000 g, 4°C). The precipitate was washed in each case with 150 µl of  
35 ethanol (70% v/v, -20°C) and dried under vacuum. Finally, the DNA was taken up in 80 µl of TE/10.

*E. coli* XL1-Blue cells were transformed with the ligated DNA by electroporation according to the

procedure described in Example 1, with in each case  
40  $\mu$ l of cell suspension of electrocompetent cells  
being mixed with 5  $\mu$ l of the DNA solution in 16  
mixtures. After electroporation, the cells were  
5 immediately diluted in 2 ml of fresh ice-cold SOC  
medium and agitated at 37°C and 200 rpm for 60 min.

168 ml of 2xYT medium and 200  $\mu$ l of ampicillin (stock  
solution 100 mg/ml, final concentration 100 mg/l) were  
10 added to the combined suspensions. The total number of  
transformants obtained was estimated at  $1.48 \cdot 10^9$  by  
plating out 100  $\mu$ l of a  $1:10^4$  dilution of the obtained  
cell suspension on agar plates. After incubation at  
37°C and 160 rpm for 60 min, the transformants were  
15 infected with 4 ml of VCS-M13 helper phage ( $6.3 \cdot 10^{11}$   
pfu/ml, Stratagene) and agitated at 37°C and 160 rpm  
for a further 30 min. Subsequently, 400  $\mu$ l of kanamycin  
(stock solution 35 mg/ml, final concentration 70 mg/l)  
were added, the incubator temperature was lowered to  
20 26°C and, after 10 min, anhydrotetracycline (100  $\mu$ l of  
a 50  $\mu$ g/ml stock solution in dimethylformamide, final  
concentration 25  $\mu$ g/l) was added to induce gene  
expression. Finally, the phagemids were produced by  
incubating the culture at 26°C and 160 rpm for 7 h. The  
25 cells were removed and the phagemids purified by  
precipitation as described in Example 1.

Streptavidin-coated paramagnetic particles (Dynabeads  
M-280 Streptavidin, Dynal) were used together with a  
30 double conjugate of BSA with digoxigenin and biotin for  
affinity enrichment from the library of phagemids which  
presented the partially mutated DigA mutein.

A double conjugate of BSA with digoxigenin and biotin  
35 was prepared by adding 1.5  $\mu$ mol (0.99 mg) of DIG-NHS in  
12.5  $\mu$ l of DMSO and 1.5  $\mu$ mol (0.68 mg) of  
D-biotinoyl- $\epsilon$ -aminocaproic acid N-hydroxysuccinimide  
ester (Boehringer Mannheim) in 12.5  $\mu$ l of DMSO in  $\mu$ l  
steps and with constant mixing to 300 nmol (19.88 mg)

of BSA in 1.9 ml of 5% w/v sodium hydrogen carbonate. The mixture was incubated with stirring at RT for 1 h. Excess reagent was removed from the double conjugate via a PD-10 gel filtration column according to the  
5 manufacturer's instructions.

In order to enrich Digoxigenin-binding phagemids, 40 µl of a 0.5 µM solution of the double conjugate (33.5 µg/ml) in PBS were mixed with 260 µl of a  
10 solution of the freshly prepared phagemids (between  $5 \cdot 10^{11}$  and  $5 \cdot 10^{12}$  cfu/ml) and incubated at RT for 1 h so that the complex formation between the digoxigenin group and the muteins presented by the phagemids was able to occur. This was followed by adding 100 µl of a  
15 solution of 8% w/v BSA, 0.4% v/v Tween 20 in PBS.

Parallel thereto, 100 µl of the commercially available suspension of paramagnetic particles were washed with three times 100 µl of PBS. Here, the particles were  
20 kept suspended for 1 min by rotating the 1.5 ml Eppendorf vessel and then collected at the wall of the Eppendorf vessel with the aid of a magnet, and the supernatant was stripped off. In order to saturate unspecific binding sites, the paramagnetic particles  
25 were incubated with 100 µl of 2% w/v BSA in PBST at RT for 1 h. After removing the supernatant, the mixture of double conjugate and phagemids was added to the paramagnetic particles, and the particles were resuspended and incubated at RT for 10 min. Finally,  
30 free biotin-binding sites of Streptavidin were saturated by adding 10 µl of a 4 µM D-desthiobiotin (Sigma) solution in PBS to the mixture and incubating said mixture at RT for 5 min. This procedure also prevented the Strep-tag II as part of the fusion  
35 protein of the muteins and the phage coat protein pIII fragment from being able to form a complex with Streptavidin.

Unbound phagemids were removed by washing the paramagnetic particles eight times with 1 ml of fresh PBST with the addition of 1 mM D-desthiobiotin, the particles were collected with the aid of the magnet and the supernatant was stripped off. The bound phagemids were eluted by incubating the resuspended particles in 950  $\mu$ l of 0.1 M glycine/HCl pH 2.2 for 15 minutes. After collecting the particles on the magnet, the supernatant was again stripped off and this was immediately followed by neutralizing the pH of said solution by addition of 140  $\mu$ l of 0.5 M Tris.

The phagemids were propagated by mixing the elution fraction obtained, according to the procedure in Example 1, with 4 ml of an exponentially growing culture of *E. coli* XL1-Blue ( $OD_{550} = 0.5$ ) and incubating at 37°C, 200 rpm for 30 min. The phagemid-infected cells were then sedimented (2 min, 4420 g, 4°C), resuspended in 800  $\mu$ l of fresh 2xYT medium and plated out on four agar plates containing LB/Amp medium (140 mm in diameter). After incubation at 32°C for 14 h, the colonies obtained in this way were scraped off the agar plates with the addition of in each case 10 ml of 2xYT/Amp medium, transferred to a sterile Erlenmeyer flask and agitated at 37°C, 200 rpm for 20 min to complete resuspension.

For repeated production and affinity enrichment of phagemid particles 50 ml of 2xYT/Amp medium prewarmed to 37°C was inoculated with 0.2 to 1 ml of said suspension so that the cell density was  $OD_{550} = 0.08$ . This culture was incubated at 37°C, 160 rpm to a cell density of  $OD_{550} = 0.5$  and infected with 300  $\mu$ l of VCS-M13 helper phage ( $6.3 \cdot 10^{11}$  pfu/ml, Stratagene). The affinity selection was then repeated using the paramagnetic particles and the digoxigenin/biotin double conjugate under the abovementioned conditions. A total of 4 selection cycles were carried out in this way.

The phagemids obtained after the last concentration cycle were again used for infecting *E. coli* XL1-Blue. The mixture of the obtained colonies which had been  
5 scraped off the agar plates using 2xYT/Amp medium and had been resuspended, as described above, was used to inoculate 50 ml of 2xYT/Amp medium, and phasmid DNA was isolated using the QIAprep spin miniprep kit (QIAGEN) according to the manufacturer's instructions.

10

Subsequently, the gene cassette between the two *Bst*XI cleavage sites was subcloned, as in Example 1, from vector pBBP24 into vector pBBP22, and competent cells of *E. coli* strain TG1-F<sup>-</sup> were transformed according to  
15 the CaCl<sub>2</sub> method. Finally, the transformants were, again according to Example 1, screened for production of muteins with binding activity for the digoxigenin group by means of the colony screening assay.

20

Seven of the colonies showing a strong signal intensity in the colony screening assay were cultured. Their plasmid DNA was isolated by means of the plasmid miniprep spin kit (Genomed) according to the manufacturer's instructions, and the gene section  
25 coding for the mutein was subjected to sequence analysis as in Example 1. It was found in the process that all plasmids studied had different sequences. After translating the nucleotide sequences into amino acid sequences, six of the seven variants studied had  
30 an amber stop codon at amino acid position 28. However, this stop codon was at least partially suppressed when choosing suitable amber-suppressor strains such as, for example, *E. coli* XL1-Blue or TG1-F<sup>-</sup> and instead translated as glutamine. Thus a full-length functional  
35 protein was produced both during affinity enrichment and in the colony screening assay.

As the only mutein without an amber stop codon among the muteins found, the mutein with SEQ ID NO:15 was

particularly well suited for bacterial production. Consequently, this mutein, also denoted by DigA16, was characterized in more detail with regard to its ability to bind to the digoxigenin group.

5

Example 3: Production of the DigA and DigA16 muteins and determination of their affinity for digoxigenin and derivatives thereof by fluorescence titration

10 For preparative production of the bilin-binding protein muteins obtained from the previous Examples the coding gene section between the two *Bst*XI cleavage sites was subcloned from the type pBBP22 vector into the expression plasmid pBBP21. The plasmid thus obtained  
15 coded for a fusion protein of the OmpA signal sequence, followed by the mutein and the Strep-tag II affinity tag.

A relevant section of the pBBP21 nucleic acid sequence  
20 is represented, together with the encoded amino acid sequence, as SEQ ID NO:16 in the sequence listing. The section starts with the *Xba*I cleavage site and ends with a hexanucleotide which was obtained by ligating a blunt strand end with a filled-up *Hind*III strand end,  
25 with the loss of the original *Hind*III cleavage site. The vector elements outside this region are identical to vector pASK75.

For subcloning, the plasmid DNA coding for the relevant  
30 mutein was cut with restriction enzyme *Bst*XI, and the smaller of the two fragments (335 bp) was purified by preparative agarose gel electrophoresis as described in Example 1. In the same manner, pBBP21 vector DNA was cut with *Bst*XI, and the larger of the two fragments  
35 (4132 bp) was isolated.

1.5 Weiss units of T4 DNA ligase (Promega) were added to 50 fmol of each of the two DNA fragments in a total volume of 20 µl (30 mM Tris/HCl pH 7.8, 10 mM MgCl<sub>2</sub>,

10 mM DTT, 1 mM ATP) and the mixture was incubated for ligation at 16°C for 16 h. 5 µl of the ligation mixture were then used to transform *E. coli* JM83 (Yanisch-Perron et al., Gene 33 (1985), 103-119) according to the CaCl<sub>2</sub> method, wherein 2.2 ml of a cell suspension were obtained. 100 µl of this suspension were plated out on an agar plate containing LB/Amp medium and incubated at 37°C for 14 h.

10 For protein production, one of the obtained single colonies was selected, a 50 ml preculture (LB/Amp medium) was inoculated with this colony and incubated at 30°C and 200 rpm overnight. 40 ml of the preculture were then transferred by inoculating 2 l of LB/Amp medium in a 5 l Erlenmeyer flask, followed by incubating the culture at 22°C and 200 rpm. At a cell density of OD<sub>550</sub> = 0.5, gene expression was induced by adding 200 µg/l anhydrotetracycline (200 µl of a 2 mg/ml stock solution in DMF), followed by agitating at 22°C, 200 rpm for a further 3 h.

The cells were removed by centrifugation (15 min, 4420 g, 4°C) and, after removing the supernatant, resuspended in 20 ml of periplasm lysis buffer (100 mM Tris/HCl pH 8.0, 500 mM sucrose, 1 mM EDTA) with cooling on ice. After incubation on ice for 30 min, the spheroplasts were removed in two successive centrifugation steps (15 min, 4420 g, 4°C and 15 min, 30 000 g, 4°C). The periplasmic protein extract obtained in this way was dialyzed against SA buffer (100 mM Tris/HCl pH 8.0, 150 mM NaCl, 1 mM EDTA), sterile-filtered and used for chromatographic purification.

35 Purification was carried out by means of the Strep-tag II affinity tag (Schmidt and Skerra, Protein Eng. 6 (1993), 109-122) fused to the C-terminus of the muteins. In the present case, Streptavidinmutedin "1" was used (Voss and Skerra, Protein Eng. 10 (1997), 975-

982), which was coupled to activated Sepharose (with 5 mg/ml immobilized Streptavidin with respect to the bed volume of the matrix).

5 A chromatography column packed with 2 ml of said material was equilibrated at 4°C and a flow rate of 20 ml/h with 10 ml of SA buffer. The chromatography was monitored by measuring absorption of the eluate at 280 nm in a flow-through photometer. Application of the  
10 periplasmic protein extract was followed by washing with SA buffer until the base line was reached. Bound mutein was then eluted with 10 ml of a solution of 2.5 mM D-desthiobiotin (Sigma) in SA buffer. The fractions containing the purified mutein were checked  
15 by means of SDS polyacrylamide gel electrophoresis (Fling and Gregerson, Anal. Biochem. 155 (1986), 83-88) and combined. The protein yields were between 200 µg and 800 µg per 2 l culture.

20 The ligand binding properties of muteins DigA, DigA16 and also of the recombinant bilin-binding protein (SEQ ID NO:16) were determined by means of the method of fluorescence titration. In this case, the decrease in intrinsic tyrosine and/or tryptophan fluorescence of  
25 the protein forming a complex with the ligand was measured. The measurements were carried out in a fluorimeter, type LS 50 B (Perkin Elmer) at an excitation wavelength of 295 nm (slit width 4 nm) and an emission wavelength of 345 nm (slit width 6 nm). The  
30 ligands used were digoxigenin (Fluka), digoxin (Fluka), digitoxigenin (Fluka), digitoxin (Fluka), testosterone (Sigma), ouabain (Fluka), and 4-aminofluorescein (Fluka). The ligands showed no significant intrinsic fluorescence or absorption at the stated wavelength.

35

The buffer system used was PBS with the addition of 1 mM EDTA. The solution of the relevant purified mutein was dialyzed four times against this buffer and adjusted to a concentration of 1 µM by dilution. All



solutions used were sterile-filtered (Filtropur S 0.45 µm, Sarstedt). The concentration was determined by means of absorption at 280 nm using calculated extinction coefficients of 53580 M<sup>-1</sup> cm<sup>-1</sup> for DigA and  
 5 DigA16 (Wisconsin Software Package, Genetics Computer Group). For Bbp, the calculated extinction coefficient of 54150 M<sup>-1</sup> cm<sup>-1</sup>, corrected in the presence of guanidinium chloride according to Gill and von Hippel (Anal. Biochem. 182 (1989), 319-326) was used.

10 For the measurement, 2 ml of the mutein solution were introduced into a quartz cuvette equipped with a magnetic stirrer bar and thermally equilibrated at 25°C in the sample holder of the photometer. Then a total of  
 15 40 µl of a 100 µM to 500 µM solution of the ligand in the same buffer were pipetted in steps of from 1 µl to 4 µl. The dilution of the introduced protein solution by altogether no more than 2%, which took place in the process, was not taken into account in the subsequent  
 20 evaluation of the data. After each titration step, the equilibrium was allowed to reach by incubating with stirring for 1 min, and the fluorescence signal was measured as average over 10 s. After subtracting the fluorescence value of the buffer, the signals were  
 25 normalized to an initial value of 100%.

The thus obtained data of a titration series were fitted by nonlinear regression using the computer program Kaleidagraph (Abelbeck Software) according to  
 30 the following equation

$$F = ([P]_t - [L]_t - K_d) \frac{f_P}{2} + ([P]_t + [L]_t + K_d) \frac{f_{PL}}{2} + (f_P - f_{PL}) \sqrt{\frac{([P]_t + [L]_t + K_d)^2}{4} - [P]_t [L]_t}$$

Here, F means the normalized fluorescence intensity and  
 35 [L]<sub>t</sub> the total ligand concentration in the particular titration step. [P]<sub>t</sub> as mutein concentration, f<sub>PL</sub> as fluorescence coefficient of the mutein-ligand complex

- 41 -

and  $K_d$  as the thermodynamic dissociation constant of said complex were fitted as free parameters to the normalized data.

5 Figure 1 represents graphically the results of the fluorescence titrations of the DigA16 mutein with the ligands digoxigenin, digitoxigenin and ouabain. It turns out that digitoxigenin is bound even tighter than digoxigenin, while no binding is observed for ouabain.

10

The values resulting from the fluorescence titrations for the dissociation constants of the complexes of the bilin-binding protein muteins and the various ligands are summarized in the following table:

15

<u>Bbp variant</u>	<u>Ligand</u>	<u><math>K_d</math> [nM]</u>
Bbp:	digoxigenin	-*
DigA:	digoxigenin	$295 \pm 37$
	digoxin	$200 \pm 34$
20 DigA16:	digoxigenin	$30.2 \pm 3.6$
	digoxin	$31.1 \pm 3.2$
	digitoxigenin	$2.8 \pm 2.7$
	digitoxin	$2.7 \pm 2.0$
	ouabain	-*
25	testosterone	-*
	4-aminofluorescein	-*

\* no detectable binding activity

30 Example 4: Preparation of fusion proteins of the DigA16 mutein and bacterial alkaline phosphatase and use for detecting digoxigenin groups in an ELISA and in a Western blot

35 In order to produce two different fusion proteins of the DigA16 mutein and bacterial alkaline phosphatase (PhoA) with different arrangement of the partners within the polypeptide chain, the two expression plasmids pBBP27 and pBBP29 were constructed by using

the molecular-biological methods familiar to the skilled worker.

pBBP27 codes for a fusion protein of PhoA including the  
5 signal sequence thereof, a short peptide linker having  
the amino acid sequence Pro-Pro-Ser-Ala, the sequence  
corresponding to the mature DigA16 mutein and the  
Strep-tag-II. A relevant section of the pBBP27 nucleic  
10 acid sequence is represented, together with the encoded  
amino acid sequence, as SEQ ID NO:17 in the sequence  
listing. The section begins with the *Xba*I cleavage site  
and ends with the *Hind*III cleavage site. The vector  
elements outside this region are identical to vector  
pBBP21.

15 pBBP29 codes for a fusion protein of DigA16 with  
preceding OmpA signal sequence, followed by the peptide  
sequence for Strep-tag II, a sequence of 5 glycine  
residues and the mature PhoA sequence without the N-  
20 terminal amino acid arginine. A relevant section of the  
pBBP29 nucleic acid sequence is represented, together  
with the encoded amino acid sequence, as SEQ ID NO:18  
in the sequence listing. The section begins with the  
*Xba*I cleavage site and ends with the *Hind*III cleavage  
25 site. The vector elements outside this region are  
identical to vector pBBP21.

Both plasmids additionally code for the bacterial  
protein disulfide isomerase DsbC on a separate cistron  
30 located in 3' direction. The plasmids are shown  
diagrammatically in Figure 2.

The fusion proteins encoded by plasmids pBBP27 and  
pBBP29 were produced analogously to the method for  
35 preparing the simple muteins, described in Example 3.  
In order to avoid complexing the metal ions from the  
active center of PhoA, lysis of the bacterial periplasm  
was carried out using EDTA-free lysis buffer.  
Polymyxin B sulfate (2 mg/ml, Sigma) was added to the

buffer as an agent destabilizing the outer cell membrane. All other buffers used for purification were likewise EDTA-free.

5 The fusion proteins purified by affinity chromatography by means of the Strep-tag II were dialyzed against PBS buffer overnight. The fusion protein yields were between 100 and 200 µg per 2 l of culture medium. The purity of the fusion proteins obtained was checked by  
10 SDS polyacrylamide gel electrophoresis, according to Example 3, and determined to be 90-95%. Subsequently, the fusion proteins were used for directly detecting conjugates of the digoxigenin group with various proteins both in a sandwich ELISA and in a Western  
15 blot.

While the conjugates used of digoxigenin with RNaseA and BSA were prepared according to Example 1, a conjugate of digoxigenin with ovalbumin (Sigma) was  
20 prepared by adding 1.5 µmol (0.99 mg) DIG-NHS in 25 µl of DMSO in µl steps and with constant mixing to 300 nmol (13.5 mg) of ovalbumin in 1.9 ml of 5% sodium hydrogen carbonate. The mixture was incubated with stirring at RT for 1 h. Excess reagent was removed from  
25 the ovalbumin conjugate via a PD-10 gel filtration column according to the manufacturer's instructions.

For detecting digoxigenin groups in a sandwich ELISA, the wells in in each case two rows of a microtiter  
30 plate (ELISA strips, 2x8 well with high binding capacity, F-type, Greiner) were filled in each case with 100 µl of a 100 µg/ml solution of the BSA-digoxigenin conjugate or the ovalbumin-digoxigenin conjugate in PBS and incubated at RT overnight. As a  
35 control, the wells of a fifth vertical row of the microtiter plate were filled with 100 µl of a 100 µg/ml solution of nonconjugated BSA (Sigma) in PBS and likewise incubated at RT overnight. After removing the solution, unoccupied binding sites were saturated with

200  $\mu$ l of a solution of 2% w/v BSA in PBST for 2 h. After washing three times with PBST, 50  $\mu$ l of a 1  $\mu$ M solution of the purified fusion protein were in each case introduced into the first well of a row, and the  
5 Tween concentration was adjusted to 0.1% v/v by adding 1  $\mu$ l of a solution of 5% v/v Tween. The subsequent wells in each row were initially charged with 50  $\mu$ l of PBST. Then, 50  $\mu$ l of the purified fusion protein were pipetted in each case into the second well, mixed and,  
10 starting therefrom, 1:2 dilutions were prepared stepwise in the other wells of the vertical row. After incubation at RT for 1 h, the wells were washed twice with PBST and twice with PBS. The fusion proteins bound to the digoxigenin groups were finally detected by  
15 means of alkaline phosphatase-catalyzed hydrolysis of p-nitrophenyl phosphate. For this purpose, 100  $\mu$ l of a solution of 0.5 mg/ml p-nitrophenyl phosphate (Amresco) in AP buffer (100 mM NaCl, 5 mM MgCl<sub>2</sub>, 100 mM Tris/HCl pH 8.8) were introduced into the wells and product  
20 formation was monitored by measuring absorption at 405 nm in a SpectraMax 250 photometer (Molecular Devices).

Figure 3 shows the result of this measurement.  
25 According to this, the digoxigenin group is recognized both as conjugate with BSA and as conjugate with ovalbumin, leading to the conclusion that binding by the DigA16 mutein is context-independent. Furthermore, both fusion proteins are active both with regard to the  
30 binding function for the digoxigenin group and enzymatically and produce, despite their different structure, almost identical signals.

In order to use the fusion proteins encoded by vectors  
35 pBBP27 and pBBP29 in a Western blot, 5  $\mu$ l of a protein mixture in PBS, whose concentration of digoxigenin-BSA conjugate, digoxigenin-ovalbumin conjugate and digoxigenin-RNaseA conjugate was simultaneously in each case 100  $\mu$ g/ml, as well as 5  $\mu$ l of a protein mixture in

PBS, whose concentration of underivatized BSA, ovalbumin and RNaseA likewise was simultaneously in each case 100 µg/ml, were first separated by SDS polyacrylamide gel electrophoresis. The protein mixture  
5 was then transferred to nitrocellulose by electrotransfer (Blake et al., Anal. Biochem. 136 (1984), 175-179). The membrane was then washed in 10 ml of PBST for three times 5 min and incubated with 10 ml of a 0.5 µM solution of in each case one of the two  
10 fusion proteins for 1 h. The membrane was then washed in 10 ml PBST for two times 5 min and in 10 ml of PBS for two times 5 min and finally gently agitated in 10 ml of AP buffer for 10 min. For the chromogenic detection reaction, the membrane was incubated in 10 ml  
15 of AP buffer to which 30 µl BCIP (50 µg/ml in dimethylformamide) and 5 µl NBT (75 µg/ml in 70% v/v dimethylformamide) had been added, and bound fusion protein was detected in this way.

20 Figure 4 shows the result of this detection method. It turns out again that binding of the digoxigenin group by the two fusion proteins is independent of the carrier protein and that both fusion proteins achieve comparable signal intensities. The same carrier  
25 proteins cause no signal whatsoever if they are not conjugated with the digoxigenin group.

Claims

1. A polypeptide selected from muteins of the bilin-binding protein, characterized in that it

5 (a) is able to bind digoxigenin or digoxigenin conjugates,

(b) does not bind ouabain, testosterone and 4-aminofluorescein and

10 (c) has an amino acid substitution at at least one of the sequence positions 28, 31, 34, 35, 36, 37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125, and 127 of the bilin-binding protein.

2. The polypeptide according to claim 1, 15 characterized in that the dissociation constant of the complex with digoxigenin is 100 nM or less.

3. The polypeptide according to claim 1 or 2, characterized in that it carries, in comparison with 20 the bilin-binding protein, at least one of the amino acid substitutions selected from Glu(28)->Gln, Lys(31)->Ala, Asn(34)->Asp, Ser(35)->His, Val(36)->Ile, Glu(37)->Thr, Asn(58)->Arg, His(60)->Ser, Ile(69)->Ser, Leu(88)->Tyr, Tyr(90)->Ile, Lys(95)->Gln, Asn(97)->Gly, 25 Tyr(114)->Phe, Lys(116)->Ser, Gln(125)->Met, and Phe(127)->Leu.

4. The polypeptide according to claim 3, characterized in that it has the amino acid sequence 30 depicted as SEQ ID NO:15.

5. The polypeptide as claimed in one or more of claims 1 to 4, characterized in that it carries at least one label group, selected from enzymatic label, 35 radioactive label, fluorescent label, chromophoric label, (bio)luminescent label or label containing haptens, biotin, metal complexes, metals or colloidal gold.

6. Fusion proteins of polypeptides according to one or more of claims 1 to 5, characterized in that an enzyme, another protein or a protein domain, a signal sequence and/or an affinity peptide is fused to the amino terminus of the polypeptide in an operable manner.

7. Fusion proteins of polypeptides according to one or more of claims 1 to 6, characterized in that an enzyme, another protein or a protein domain, a targeting sequence and/or an affinity peptide is fused to the carboxy terminus of the polypeptide in an operable manner.

8. A nucleic acid, characterized in that it comprises a sequence coding for a mutein or a fusion protein of a mutein of the bilin-binding protein according to one or more of claims 1 to 7.

9. The nucleic acid according to claim 8, characterized in that it comprises the nucleotide sequence according to SEQ ID NO:15 or another nucleotide sequence encoding the polypeptide according to SEQ ID NO:15.

10. A method for producing digoxigenin-binding muteins of the bilin-binding protein, which comprises the following steps:

(a) subjecting the bilin-binding protein to random mutagenesis at at least one of the sequence positions 28, 31, 34, 35, 36, 37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125, and 127,

(b) enriching resulting muteins with binding affinity for the digoxigenin group by selection and isolating said muteins,

(c) subjecting the muteins obtained in step (b) to another random mutagenesis at at least one of the sequence positions 28, 31, 34, 35, 36, and 37, and



(d) again enriching the resulting muteins by selection and isolating said muteins.

11. The method according to claim 10, wherein in  
5 step (b) selection is carried out by competitive enrichment.

12. The method according to claim 11, wherein  
free digoxigenin or digitoxigenin is used for  
10 competitive enrichment.

13. The method according to any of claims 10 to  
12, wherein the enrichment in step (d) is carried out  
by forming a complex of the muteins with the  
15 digoxigenin group and subsequently dissociating the  
complex.

14. The method according to claim 13, wherein the  
dissociation of the complex of mutein and digoxigenin  
20 group is carried out in acidic or basic medium milieu.

15. A method for preparing a mutein or a fusion  
protein of a mutein of the bilin-binding protein  
according to one or more of claims 1 to 7 or for  
25 preparing a mutein which is obtainable according to a  
method according to one or more of claims 10 to 14,  
characterized in that the nucleic acid coding for the  
mutein or the fusion protein of a mutein of the bilin-  
binding protein is expressed in a bacterial or  
30 eukaryotic host cell and the polypeptide is obtained  
from the cell or the culture supernatant.

15. The use of a mutein or a fusion protein of a  
mutein of the bilin-binding protein according to one or  
35 more of claims 1 to 7 or of a mutein which is  
obtainable according to a method according to one or  
more of claims 10 to 14 for binding, detecting,  
determining, immobilizing or removing digoxigenin or  
conjugates of digoxigenin with proteins, nucleic acids,

2

15

Abstract

The present invention relates to muteins of the bilin-binding protein with binding activity to digoxigenin and to fusion proteins of such muteins, a method for  
5 preparing said muteins and fusion proteins thereof and their utilization for detecting or binding digoxigenin-labeled biomolecules. The invention especially relates to a polypeptide selected from muteins of the bilin-  
10 binding protein, characterized in that (a) it can bind digoxigenin or digoxigenin conjugates, (b) it does not bind ouabain, testosterone, and 4-aminofluorescein and (c) at least one of the sequence positions 28, 31, 34, 35, 36, 37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125,  
15 and 127 of the bilin-binding protein has an amino acid substitution. Due to their simple molecular structure, the inventive muteins provide advantages for production and utilization in comparison with antibodies against the digoxigenin group.

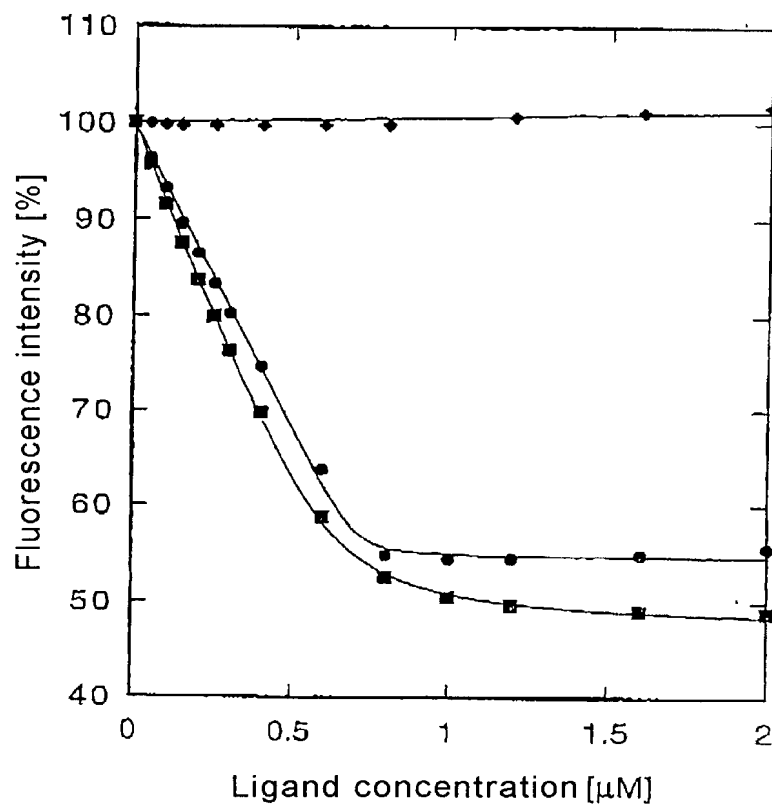
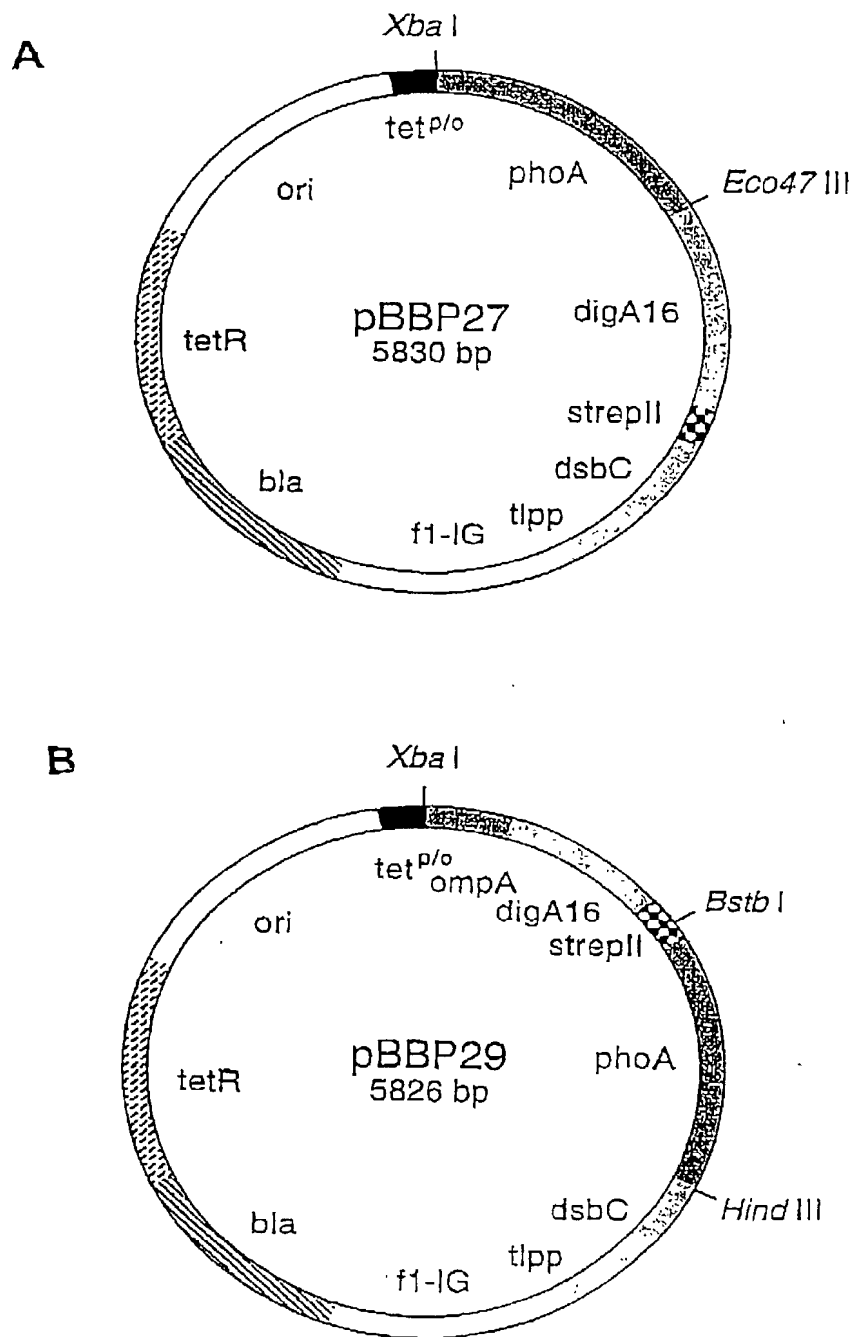


Figure 1

2/4



**Figure 2**

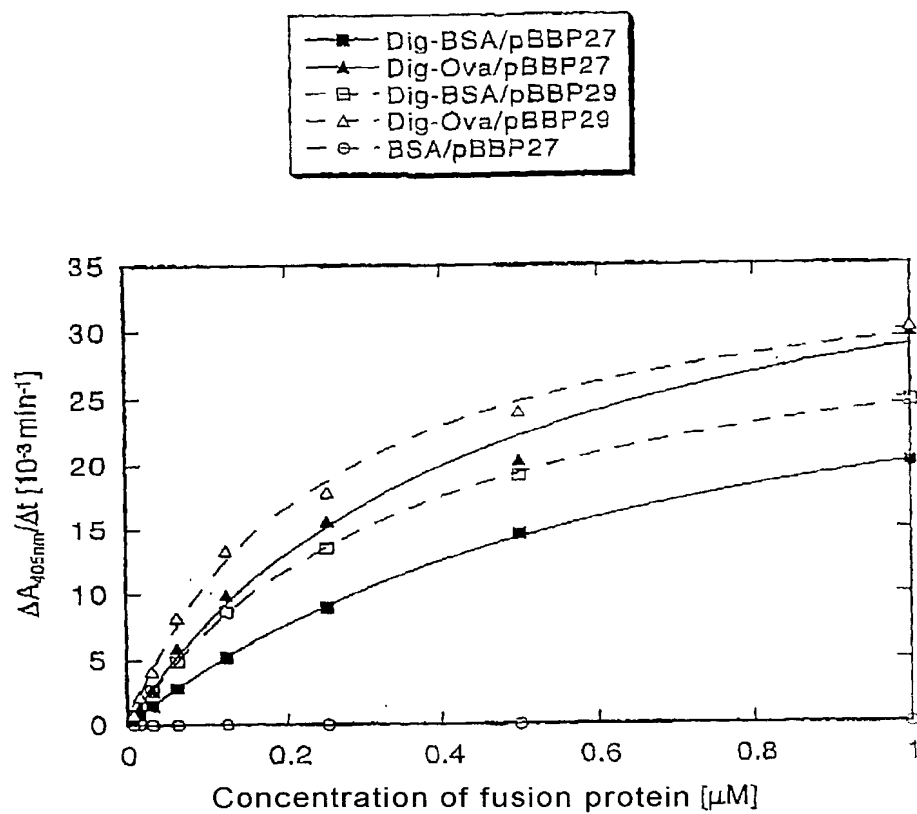


Figure 3

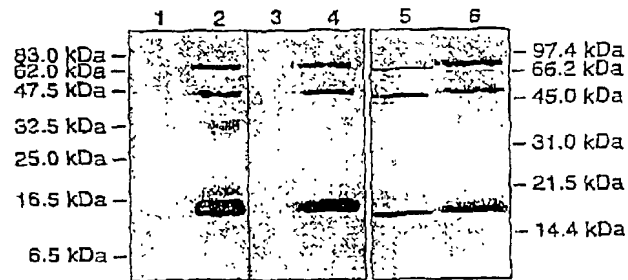


Figure 4

09/980862 09/980862

09/980862

JC10 Rec'd PGT/PTO 07 DEC 2001

1

SEQUENCE LISTINGS

<110> Skerra, Arne, Prof. Dr.

5. <120> Muteins of bilin-binding protein

<150> DE 199 26 068.0

<151> 1999-06-08

10 <160> 18

<210> 1

<211> 1219 base pairs

<212> DNA

15 <213> artificial sequence

<220>

<221> sig\_peptide

<222> (22)...(84)

20

<220>

<221> mat\_peptide

<222> (85)...(1209)

<223> fusion protein of bilin-binding protein, Strep-tag II und fragment

25 of phage coat protein pIII

<220>

<221> CDS

<222> (85)...(606)

30 <223> mature bilin-binding protein

<220>

<221> CDS

<222> (607)...(636)

35 <223> Strep-tag II-affinity tag

<220>

<221> CDS



<222> (637)...(639)

<223> amber stop codon

<220>

5 <221> CDS

<222> (640)...(1209)

<223> amino acids 217-406 of coat protein pIII

<400> 1

```

10 TCTAGTTAAC GAGGGCAAAA A ATG AAA AAG ACA GCT ATC GCG ATT      45
    Met Lys Lys Thr Ala Ile Ala Ile
    -21 -20 -15

15 GCA GTG GCA CTG GCT GGT TTC GCT ACC GTA GCG CAG GCC GAC GTG   90
    Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val
    -10 -5 -1 1

20 TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA GTC GAC AAC TTC 135
    Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe
    5 10 15

25 GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG GAA GTC GCC AAA TAC 180
    Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr
    20 25 30

30 CCC AAC TCA GTT GAG AAG TAC GGA AAG TGC GGA TGG GCT GAG TAC 225
    Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr
    35 40 45

35 ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG AAC TAC CAC GTA ATC 270
    Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val Ile
    50 55 60

40 CAC GGC AAG GAA TAC TTT ATT GAA GGA ACT GCC TAC CCA GTT GGT 315
    His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly
    65 70 75

45 GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC CTG ACT TAC GGA GGT 360
    Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly
    80 85 90

50 GTC ACC AAG GAG AAC GTA TTC AAC GTA CTC TCC ACT GAC AAC AAG 405
    Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys
    95 100 105

AAC TAC ATC ATC GGA TAC TAC TGC AAA TAC GAC GAG GAC AAG AAG 450
    Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys
    110 115 120

GGA CAC CAA GAC TTC GTC TGG GTG CTC TCC AGA AGC ATG GTC CTT 495
    Gly His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu
    125 130 135

```

	ACT	GGT	GAA	GCC	AAG	ACC	GCT	GTC	GAG	AAC	TAC	CTT	ATC	GGC	TCC	540
	Thr	Gly	Glu	Ala	Lys	Thr	Ala	Val	Glu	Asn	Tyr	Leu	Ile	Gly	Ser	
			140					145					150			
5	CCA	GTA	GTC	GAC	TCC	CAG	AAA	CTG	GTA	TAC	AGT	GAC	TTC	TCT	GAA	585
	Pro	Val	Val	Asp	Ser	Gln	Lys	Leu	Val	Tyr	Ser	Asp	Phe	Ser	Glu	
			155					160					165			
10	GCC	GCC	TGC	AAG	GTC	AAC	AAT	AGC	AAC	TGG	TCT	CAC	CCG	CAG	TTC	630
	Ala	Ala	Cys	Lys	Val	Asn	Asn	Ser	Asn	Trp	Ser	His	Pro	Gln	Phe	
			170					175					180			
15	GAA	AAA	TAG	GCT	GGC	GGC	GGC	TCT	GGT	GGT	GGT	TCT	GGC	GGC	GGC	675
	Glu	Lys	Gln	Ala	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
			185					190					195			
20	TCT	GAG	GGT	GGT	GGC	TCT	GAG	GGT	GGC	GGT	TCT	GAG	GGT	GGC	GGC	720
	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	
			200					205					210			
25	TCT	GAG	GGA	GGC	GGT	TCC	GGT	GGT	GGC	TCT	GGT	TCC	GGT	GAT	TTT	765
	Ser	Glu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	
			215					220					225			
30	GAT	TAT	GAA	AAG	ATG	GCA	AAC	GCT	AAT	AAG	GGG	GCT	ATG	ACC	GAA	810
	Asp	Tyr	Glu	Lys	Met	Ala	Asn	Ala	Asn	Lys	Gly	Ala	Met	Thr	Glu	
			230					235					240			
35	AAT	GCC	GAT	GAA	AAC	GCG	CTA	CAG	TCT	GAC	GCT	AAA	GGC	AAA	CTT	855
	Asn	Ala	Asp	Glu	Asn	Ala	Leu	Gln	Ser	Asp	Ala	Lys	Gly	Lys	Leu	
			245					250					255			
40	GAT	TCT	GTC	GCT	ACT	GAT	TAC	GGT	GCT	GCT	ATC	GAT	GGT	TTC	ATT	900
	Asp	Ser	Val	Ala	Thr	Asp	Tyr	Gly	Ala	Ala	Ile	Asp	Gly	Phe	Ile	
			260					265					270			
45	GGT	GAC	GTT	TCC	GGC	CTT	GCT	AAT	GGT	AAT	GGT	GCT	ACT	GGT	GAT	945
	Gly	Asp	Val	Ser	Gly	Leu	Ala	Asn	Gly	Asn	Gly	Ala	Thr	Gly	Asp	
			275					280					285			
50	TTT	GCT	GGC	TCT	AAT	TCC	CAA	ATG	GCT	CAA	GTC	GGT	GAC	GGT	GAT	990
	Phe	Ala	Gly	Ser	Asn	Ser	Gln	Met	Ala	Gln	Val	Gly	Asp	Gly	Asp	
			290					295					300			
55	AAT	TCA	CCT	TTA	ATG	AAT	AAT	TTC	CGT	CAA	TAT	TTA	CCT	TCC	CTC	1035
	Asn	Ser	Pro	Leu	Met	Asn	Asn	Phe	Arg	Gln	Tyr	Leu	Pro	Ser	Leu	
			305					310					315			
60	CCT	CAA	TCG	GTT	GAA	TGT	CGC	CCT	TTT	GTC	TTT	GGC	GCT	GGT	AAA	1080
	Pro	Gln	Ser	Val	Glu	Cys	Arg	Pro	Phe	Val	Phe	Gly	Ala	Gly	Lys	
			320					325					330			
65	CCA	TAT	GAA	TTT	TCT	ATT	GAT	TGT	GAC	AAA	ATA	AAC	TTA	TTC	CGT	1125
	Pro	Tyr	Glu	Phe	Ser	Ile	Asp	Cys	Asp	Lys	Ile	Asn	Leu	Phe	Arg	
			335					340					345			
70	GGT	GTC	TTT	GCG	TTT	CTT	TTA	TAT	GTT	GCC	ACC	TTT	ATG	TAT	GTA	1170
	Gly	Val	Phe	Ala	Phe	Leu	Leu	Tyr	Val	Ala	Thr	Phe	Met	Tyr	Val	
			350					355					360			

TTT TCT ACG TTT GCT AAC ATA CTG CGT AAT AAG GAG TCT 1209  
Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser  
365 370 375

5 TAATAAGCTT 1219

<210> 2

<211> 64 bases

10 <212> DNA

<213> artificial sequence

<220>

<223> primer

15

<400> 2

CCATGGTAAA TGGTGGGAAG TCGCCAAATA CCCCNKNMS NNSNNKAAGT 50  
ACGGAAAGTG CGGA 64

20

<210> 3

<211> 71 bases

<212> DNA

25 <213> artificial sequence

<220>

<223> primer

30

<400> 3

GGGTAGGCGG TACCTTCSNN AAAGTATTCC TTGCCGTGGA TTACMNGTA 50  
SNNCGAAACT TTGACACTCT T 71

35

<210> 4

<211> 74 bases

<212> DNA

<213> artificial sequence

40

<220>

<223> primer

<400> 4

5 CCAAGATTGG AAAGATCTAC CACAGCNNSA CTNNKGGAGG TNNSACCVVS 50  
GAGNNKGTAT TCAACGTACT CTCC 74

<210> 5

<211> 78 bases

10 <212> DNA

<213> artificial sequence

<220>

<223> primer

15

<400> 5

TCTGGAGAGC ACCCAGACMN NGTCSNNGTG TCCCTTCTTG TCCTCGTCGT 50  
ASNNGCAMNN GTATCCGATG ATGTAGTT 78

20

<210> 6

<211> 36 bases

<212> DNA

<213> artificial sequence

25

<220>

<223> primer

<400> 6

30

CTTCGACTGG TCCCAGTACC ATGGTAAATG GTGGGA 36

<210> 7

35

<211> 37 bases

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 7

CACCAGTAAG GACCATGCTT CTGGAGAGCA CCCAGAC 37

5

<210> 8

<211> 46 bases

<212> DNA

<213> artificial sequence

10

<220>

<223> synthetic oligodeonucleotide

<400> 8

15 AGATCTTTCC AATCTTGGAG TCACCAACTG GGTAGGCGGT ACCTTC 46

<210> 9

<211> 793 base pairs

20

<212> DNA

<213> fragment of plasmid pBBP22

<220>

<221> sig\_peptide

25

<222> (22)...(84)

<220>

<221> mat\_peptide

<222> (85)...(783)

30

<223> fusion protein of bilin-binding protein, Strep-Tag II und albumin-binding domain

<220>

<221> CDS

35

<222> (85)...(606)

<223> mature bilin-binding protein

<220>

<221> CDS

<222> (607)...(636)

<223> Strep-Tag II affinity tag

5

<220>

<221> CDS

<222> (637)...(783)

<223> albumin binding domain from Protein G

10

<400> 9

	TCTAGATAAC	GAGGGCAAAA	A	ATG	AAA	AAG	ACA	GCT	ATC	GCG	ATT		45			
				Met	Lys	Lys	Thr	Ala	Ile	Ala	Ile					
15				-21	-20					-15						
	GCA	GTG	GCA	CTG	GCT	GGT	TTC	GCT	ACC	GTA	GCG	CAG	GCC	GAC	GTG	90
	Ala	Val	Ala	Leu	Ala	Gly	Phe	Ala	Thr	Val	Ala	Gln	Ala	Asp	Val	
				-10				-5				-1	1			
20	TAC	CAC	GAC	GGT	GCC	TGT	CCC	GAA	GTC	AAG	CCA	GTC	GAC	AAC	TTC	135
	Tyr	His	Asp	Gly	Ala	Cys	Pro	Glu	Val	Lys	Pro	Val	Asp	Asn	Phe	
			5					10					15			
25	GAC	TGG	TCC	CAG	TAC	CAT	GGT	AAA	TGG	TGG	GAA	GTC	GCC	AAA	TAC	180
	Asp	Trp	Ser	Gln	Tyr	His	Gly	Lys	Trp	Trp	Glu	Val	Ala	Lys	Tyr	
			20					25					30			
30	CCC	AAC	TCA	GTT	GAG	AAG	TAC	GGA	AAG	TGC	GGA	TGG	GCT	GAG	TAC	225
	Pro	Asn	Ser	Val	Glu	Lys	Tyr	Gly	Lys	Cys	Gly	Trp	Ala	Glu	Tyr	
			35					40					45			
35	ACT	CCT	GAA	GGC	AAG	AGT	GTC	AAA	GTT	TCG	AAC	TAC	CAC	GTA	ATC	270
	Thr	Pro	Glu	Gly	Lys	Ser	Val	Lys	Val	Ser	Asn	Tyr	His	Val	Ile	
			50					55					60			
40	CAC	GGC	AAG	GAA	TAC	TTT	ATT	GAA	GGA	ACT	GCC	TAC	CCA	GTT	GGT	315
	His	Gly	Lys	Glu	Tyr	Phe	Ile	Glu	Gly	Thr	Ala	Tyr	Pro	Val	Gly	
			65					70					75			
45	GAC	TCC	AAG	ATT	GGA	AAG	ATC	TAC	CAC	AGC	CTG	ACT	TAC	GGA	GGT	360
	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	His	Ser	Leu	Thr	Tyr	Gly	Gly	
			80					85					90			
50	GTC	ACC	AAG	GAG	AAC	GTA	TTC	AAC	GTA	CTC	TCC	ACT	GAC	AAC	AAG	405
	Val	Thr	Lys	Glu	Asn	Val	Phe	Asn	Val	Leu	Ser	Thr	Asp	Asn	Lys	
			95					100					105			
50	AAC	TAC	ATC	ATC	GGA	TAC	TAC	TGC	AAA	TAC	GAC	GAG	GAC	AAG	AAG	450
	Asn	Tyr	Ile	Ile	Gly	Tyr	Tyr	Cys	Lys	Tyr	Asp	Glu	Asp	Lys	Lys	
			110					115					120			

GGA CAC CAA GAC TTC GTC TGG GTG CTC TCC AGA AGC ATG GTC CTT 495  
 Gly His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu  
 125 130 135  
 5 ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC GGC TCC 540  
 Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser  
 140 145 150  
 10 CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC TCT GAA 585  
 Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu  
 155 160 165  
 15 GCC GCC TGC AAG GTC AAC AAT AGC AAC TGG TCT CAC CCG CAG TTC 630  
 Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe  
 170 175 180  
 GAA AAA CCA GCT AGC CTG GCT GAA GCT AAA GTT CTG GCT AAC CGT 675  
 Glu Lys Pro Ala Ser Leu Ala Glu Ala Lys Val Leu Ala Asn Arg  
 185 190 195  
 20 GAA CTG GAC AAA TAC GGT GTT TCC GAC TAC TAC AAA AAC CTC ATC 720  
 Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile  
 200 205 210  
 25 AAC AAC GCT AAA ACC GTT GAA GGT GTT AAA GCT CTG ATC GAC GAA 765  
 Asn Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu Ile Asp Glu  
 215 220 225  
 30 ATT CTC GCA GCA CTG CCG TAATAAGCTT 793  
 Ile Leu Ala Ala Leu Pro  
 230

<210> 10

35 <211> 17 bases

<212> DNA

<213> artificial sequence

<220>

40 <223> sequencing primer

<400> 10

GACGGTGCCT GTCCCGA 17

45 <210> 11

<211> 17 bases

<212> DNA

<213> artificial sequence

<220>

<223> sequencing primer

<400> 11

5

GACTACTGGG GAGCCGA 17

<210> 12

10 <211> 522 bases

<212> DNA

<213> coding sequence of mutein DigA

<220>

15 <221> CDS

<222> (1)...(522)

<223> mutein DigA without fusions parts

<400> 12

20

GAC	GTG	TAC	CAC	GAC	GGT	GCC	TGT	CCC	GAA	GTC	AAG	CCA	GTC	GAC	45
Asp	Val	Tyr	His	Asp	Gly	Ala	Cys	Pro	Glu	Val	Lys	Pro	Val	Asp	
1				5					10					15	

25

AAC	TTC	GAC	TGG	TCC	CAG	TAC	CAT	GGT	AAA	TGG	TGG	GAA	GTC	GCC	90
Asn	Phe	Asp	Trp	Ser	Gln	Tyr	His	Gly	Lys	Trp	Trp	Glu	Val	Ala	
				20					25					30	

30

AAA	TAC	CCC	CAT	CAC	GAG	CGG	AAG	TAC	GGA	AAG	TGC	GGA	TGG	GCT	135
Lys	Tyr	Pro	His	His	Glu	Arg	Lys	Tyr	Gly	Lys	Cys	Gly	Trp	Ala	
				35					40					45	

35

GAG	TAC	ACT	CCT	GAA	GGC	AAG	AGT	GTC	AAA	GTT	TCG	CGC	TAC	TCT	180
Glu	Tyr	Thr	Pro	Glu	Gly	Lys	Ser	Val	Lys	Val	Ser	Arg	Tyr	Ser	
				50					55					60	

40

GTA	ATC	CAC	GGC	AAG	GAA	TAC	TTT	TCC	GAA	GGT	ACC	GCC	TAC	CCA	225
Val	Ile	His	Gly	Lys	Glu	Tyr	Phe	Ser	Glu	Gly	Thr	Ala	Tyr	Pro	
				65					70					75	

GTT	GGT	GAC	TCC	AAG	ATT	GGA	AAG	ATC	TAC	CAC	AGC	TAC	ACT	ATT	270
Val	Gly	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	His	Ser	Tyr	Thr	Ile	
				80					85					90	

45

GGA	GGT	GTG	ACC	CAG	GAG	GGT	GTA	TTC	AAC	GTA	CTC	TCC	ACT	GAC	315
Gly	Gly	Val	Thr	Gln	Glu	Gly	Val	Phe	Asn	Val	Leu	Ser	Thr	Asp	
				95					100					105	



10

AAC AAG AAC TAC ATC ATC GGA TAC TTT TGC TCG TAC GAC GAG GAC 360  
Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp Glu Asp  
110 115 120

5 AAG AAG GGA CAC ATG GAC TTG GTC TGG GTG CTC TCC AGA AGC ATG 405  
Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg Ser Met  
125 130 135

10 GTC CTT ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC 450  
Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile  
140 145 150

15 GGC TCC CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC 495  
Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe  
155 160 165

TCT GAA GCC GCC TGC AAG GTC AAC AAT 522  
Ser Glu Ala Ala Cys Lys Val Asn Asn  
170

20

<210> 13

<211> 76 bases

<212> DNA

25 <213> artificial sequence

<220>

<223> primer

30 <400> 13

CTGGTCCCAG TACCATGGTA AATGGTGGNN KGTCGCCNNK TACCCCNKN 50  
NKNNKNNKAA GTACGGAAAG TGCGGA 76

35

<210> 14

<211> 1219 bases pairs

<212> DNA

<213> fragment of phasmids pBBP24

40

<220>

<221> sig\_peptide

<222> (22)...(84)

11

<220>

<221> mat\_peptide

<222> (85)...(1209)

<223> fusion protein of bilin-binding protein, Strep-Tag II and fragment  
5 of phage coat protein pIII, with interrupted reading frame

<220>

<221> CDS

<222> (85)...(606)

10 <223> mature bilin-binding protein with interrupted reading frame

<220>

<221> CDS

<222> (607)...(636)

15 <223> Strep-Tag II affinity tag

<220>

<221> CDS

<222> (637)...(639)

20 <223> amber stop codon

<220>

<221> CDS

<222> (640)...(1209)

25 <223> amino acids 217-406 of coat protein pIII

<400> 14

30	TCTAGATAAC GAGGGCAAAA A ATG AAA AAG ACA GCT ATC GCG ATT	45
	Met Lys Lys Thr Ala Ile Ala Ile	
	-21 -20 -15	
	GCA GTG GCA CTG GCT GGT TTC GCT ACC GTA GCG CAG GCC GAC GTG	90
35	Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val	
	-10 -5 -1 1	
	TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA GTC GAC AAC TTC	135
	Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe	
	5 10 15	
40	GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG GAA GTC GCC AAA TAC	180
	Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr	
	20 25 30	

	CCC	AAC	TCA	GTT	GAG	AAG	TAC	GGA	AAT	TAA	TGA	TGG	GCT	GAG	TAC	225
	Pro	Asn	Ser	Val	Glu	Lys	Tyr	Gly	Asn			Trp	Ala	Glu	Tyr	
			35					40					45			
5	ACT	CCT	GAA	GGC	AAG	AGT	GTC	AAA	GTT	TCG	AAC	TAC	CAC	GTA	ATC	270
	Thr	Pro	Glu	Gly	Lys	Ser	Val	Lys	Val	Ser	Asn	Tyr	His	Val	Ile	
			50					55					60			
10	CAC	GGC	AAG	GAA	TAC	TTT	ATT	GAA	GGA	ACT	GCC	TAC	CCA	GTT	GGT	315
	His	Gly	Lys	Glu	Tyr	Phe	Ile	Glu	Gly	Thr	Ala	Tyr	Pro	Val	Gly	
			65					70					75			
15	GAC	TCC	AAG	ATT	GGA	AAG	ATC	TAC	CAC	AGC	CTG	ACT	TAC	GGA	GGT	360
	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	His	Ser	Leu	Thr	Tyr	Gly	Gly	
			80					85					90			
20	GTC	ACC	AAG	GAG	AAC	GTA	TTC	AAC	GTA	CTC	TCC	ACT	GAC	AAC	AAG	405
	Val	Thr	Lys	Glu	Asn	Val	Phe	Asn	Val	Leu	Ser	Thr	Asp	Asn	Lys	
			95					100					105			
25	AAC	TAC	ATC	ATC	GGA	TAC	TAC	TGC	AAA	TAC	GAC	GAG	GAC	AAG	AAG	450
	Asn	Tyr	Ile	Ile	Gly	Tyr	Tyr	Cys	Lys	Tyr	Asp	Glu	Asp	Lys	Lys	
			110					115					120			
30	GGA	CAC	CAA	GAC	TTC	GTC	TGG	GTG	CTC	TCC	AGA	AGC	ATG	GTC	CTT	495
	Gly	His	Gln	Asp	Phe	Val	Trp	Val	Leu	Ser	Arg	Ser	Met	Val	Leu	
			125					130					135			
35	ACT	GGT	GAA	GCC	AAG	ACC	GCT	GTC	GAG	AAC	TAC	CTT	ATC	GGC	TCC	540
	Thr	Gly	Glu	Ala	Lys	Thr	Ala	Val	Glu	Asn	Tyr	Leu	Ile	Gly	Ser	
			140					145					150			
40	CCA	GTA	GTC	GAC	TCC	CAG	AAA	CTG	GTA	TAC	AGT	GAC	TTC	TCT	GAA	585
	Pro	Val	Val	Asp	Ser	Gln	Lys	Leu	Val	Tyr	Ser	Asp	Phe	Ser	Glu	
			155					160					165			
45	GCC	GCC	TGC	AAG	GTC	AAC	AAT	AGC	AAC	TGG	TCT	CAC	CCG	CAG	TTC	630
	Ala	Ala	Cys	Lys	Val	Asn	Asn	Ser	Asn	Trp	Ser	His	Pro	Gln	Phe	
			170					175					180			
50	GAA	AAA	TAG	GCT	GGC	GGC	GGC	TCT	GGT	GGT	GGT	TCT	GGC	GGC	GGC	675
	Glu	Lys	Gln	Ala	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
			185					190					195			
55	TCT	GAG	GGT	GGT	GGC	TCT	GAG	GGT	GGC	GGT	TCT	GAG	GGT	GGC	GGC	720
	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	
			200					205					210			
60	TCT	GAG	GGA	GGC	GGT	TCC	GGT	GGT	GGC	TCT	GGT	TCC	GGT	GAT	TTT	765
	Ser	Glu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	
			215					220					225			
65	GAT	TAT	GAA	AAG	ATG	GCA	AAC	GCT	AAT	AAG	GGG	GCT	ATG	ACC	GAA	810
	Asp	Tyr	Glu	Lys	Met	Ala	Asn	Ala	Asn	Lys	Gly	Ala	Met	Thr	Glu	
			230					235					240			
70	AAT	GCC	GAT	GAA	AAC	GCG	CTA	CAG	TCT	GAC	GCT	AAA	GGC	AAA	CTT	855
	Asn	Ala	Asp	Glu	Asn	Ala	Leu	Gln	Ser	Asp	Ala	Lys	Gly	Lys	Leu	
			245					250					255			

5 GAT TCT GTC GCT ACT GAT TAC GGT GCT GCT ATC GAT GGT TTC ATT 900  
 Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile  
 260 265 270

10 GGT GAC GTT TCC GGC CTT GCT AAT GGT AAT GGT GCT ACT GGT GAT 945  
 Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp  
 275 280 285

15 TTT GCT GGC TCT AAT TCC CAA ATG GCT CAA GTC GGT GAC GGT GAT 990  
 Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp  
 290 295 300

20 AAT TCA CCT TTA ATG AAT AAT TTC CGT CAA TAT TTA CCT TCC CTC 1035  
 Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu  
 305 310 315

25 CCT CAA TCG GTT GAA TGT CGC CCT TTT GTC TTT GGC GCT GGT AAA 1080  
 Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys  
 320 325 330

30 CCA TAT GAA TTT TCT ATT GAT TGT GAC AAA ATA AAC TTA TTC CGT 1125  
 Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg  
 335 340 345

35 GGT GTC TTT GCG TTT CTT TTA TAT GTT GCC ACC TTT ATG TAT GTA 1170  
 Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val  
 350 355 360

40 TTT TCT ACG TTT GCT AAC ATA CTG CGT AAT AAG GAG TCT 1209  
 Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser  
 365 370 375

45 TAATAAGCTT 1219

<210> 15  
 <211> 522 bases pairs  
 <212> DNA  
 <213> coding sequence of mutein DigA16

<220>  
 <221> CDS

45 <222> (1)...(522)  
 <223> mutein DigA16 without fusion parts

<400> 15

50 GAC GTG TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA GTC GAC 45  
 Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp

14

	1	5	10	15	
	AAC TTC GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG CAG GTC GCC				90
	Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala				
5		20	25	30	
	GCG TAC CCC GAT CAT ATT ACG AAG TAC GGA AAG TGC GGA TGG GCT				135
	Ala Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala				
10		35	40	45	
	GAG TAC ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG CGC TAC TCT				180
	Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser				
		50	55	60	
15	GTA ATC CAC GGC AAG GAA TAC TTT TCC GAA GGT ACC GCC TAC CCA				225
	Val Ile His Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro				
		65	70	75	
	GTT GGT GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC TAC ACT ATT				270
20	Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile				
		80	85	90	
	GGA GGT GTG ACC CAG GAG GGT GTA TTC AAC GTA CTC TCC ACT GAC				315
	Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val Leu Ser Thr Asp				
25		95	100	105	
	AAC AAG AAC TAC ATC ATC GGA TAC TTT TGC TCG TAC GAC GAG GAC				360
	Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp Glu Asp				
		110	115	120	
30	AAG AAG GGA CAC ATG GAC TTG GTC TGG GTG CTC TCC AGA AGC ATG				405
	Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg Ser Met				
		125	130	135	
35	GTC CTT ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC				450
	Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile				
		140	145	150	
40	GGC TCC CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC				495
	Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe				
		155	160	165	
	TCT GAA GCC GCC TGC AAG GTC AAC AAT				522
45	Ser Glu Ala Ala Cys Lys Val Asn Asn				
		170			

<210> 16

<211> 1380 base pairs

50 <212> DNA

<213> fragment of plasmids PBBP21

<220>

<221> sig\_peptide

<222> (22)...(84)

<220>

<221> mat\_peptide

5 <222> (85)...(636)

<223> fusion protein of bilin-binding protein and Strep-Tag II

<220>

<221> sig\_peptide

10 <222> (658)...(717)

<220>

<221> mat\_peptide

<222> (718)...(1365)

15 <223> DsbC protein

<400> 16

20	TCTAGATAAC GAGGGCAAAA A ATG AAA AAG ACA GCT ATC GCG ATT	45
	Met Lys Lys Thr Ala Ile Ala Ile	
	-21 -20 -15	
25	GCA GTG GCA CTG GCT GGT TTC GCT ACC GTA GCG CAG GCC GAC GTG	90
	Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val	
	-10 -5 -1 1	
30	TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA GTC GAC AAC TTC	135
	Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe	
	5 10 15	
35	GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG GAA GTC GCC AAA TAC	180
	Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr	
	20 25 30	
40	CCC AAC TCA GTT GAG AAG TAC GGA AAG TGC GGA TGG GCT GAG TAC	225
	Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr	
	35 40 45	
45	ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG AAC TAC CAC GTA ATC	270
	Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val Ile	
	50 55 60	
50	CAC GGC AAG GAA TAC TTT ATT GAA GGA ACT GCC TAC CCA GTT GGT	315
	His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly	
	65 70 75	
55	GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC CTG ACT TAC GGA GGT	360
	Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly	
	80 85 90	



CAA ATG GCA GAC TAC AAC GCG CTG GGG ATC ACC GTG CGT TAT CTT 1080  
 Gln Met Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu  
 110 115 120

5 GCT TTC CCG CGC CAG GGG CTG GAC AGC GAT GCA GAG AAA GAA ATG 1125  
 Ala Phe Pro Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met  
 125 130 135

10 AAA GCT ATC TGG TGT GCG AAA GAT AAA AAC AAA GCG TTT GAT GAT 1170  
 Lys Ala Ile Trp Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp  
 140 145 150

15 GTG ATG GCA GGT AAA AGC GTC GCA CCA GCC AGT TGC GAC GTG GAT 1215  
 Val Met Ala Gly Lys Ser Val Ala Pro Ala Ser Cys Asp Val Asp  
 155 160 165

20 ATT GCC GAC CAT TAC GCA CTT GGC GTC CAG CTT GGC GTT AGC GGT 1260  
 Ile Ala Asp His Tyr Ala Leu Gly Val Gln Leu Gly Val Ser Gly  
 170 175 180

25 ACT CCG GCA GTT GTG CTG AGC AAT GGC ACA CTT GTT CCG GGT TAC 1305  
 Thr Pro Ala Val Val Leu Ser Asn Gly Thr Leu Val Pro Gly Tyr  
 185 190 195

CAG CCG CCG AAA GAG ATG AAA GAA TTC CTC GAC GAA CAC CAA AAA 1350  
 Gln Pro Pro Lys Glu Met Lys Glu Phe Leu Asp Glu His Gln Lys  
 200 205 210

30 ATG ACC AGC GGT AAA TAATTCGCGT AGCTT 1380  
 Met Thr Ser Gly Lys  
 215

35 <210> 17  
 <211> 2009 bases pairs  
 <212> DNA  
 <213> fragment of plasmid PBBP27

40 <220>  
 <221> sig\_peptide  
 <222> (23)...(85)

45 <220>  
 <221> mat\_peptide  
 <222> (86)...(1999)  
 <223> fusion protein of alkaline phosphatase, linker peptide Pro-Pro-Ser-  
 Ala, mutein DigA16 and Strep-Tag II



$\langle 220 \rangle$ 

<221> CDS

 $\langle 222 \rangle \quad (86) \dots (1435)$ 

5 <223> mature part of alkaline phosphatase

 $\langle 220 \rangle$ 

&lt;221&gt; CDS

 $\langle 222 \rangle \quad (1436) \dots (1447)$ 

10 <223> linker peptide Pro-Pro-Ser-Ala

 $\langle 220 \rangle$ 

&lt;221&gt; CDS

<222> (1448) ... (1969)

15 <223> mutein DigA16

 $\langle 220 \rangle$ 

&lt;221&gt; CDS

&lt;222&gt; (1970) . . . (1999)

20 <223> Strep-Tag II affinity tag

<400> 17

25 TCTAGAACAT GGAGAAAATA AA GTG AAA CAA AGC ACT ATT GCA CTG 46  
Val Lys Gln Ser Thr Ile Ala Leu  
-21 -20 -15

30 GCA CTC TTA CCG TTA CTG TTT ACC CCT GTG ACA AAA GCC CGG ACA 91  
Ala Leu Leu Pro Leu Leu Phe Thr Pro Val Thr Lys Ala Arg Thr  
-10 -5 -1 1

CCA GAA ATG CCT GTT CTG GAA AAC CGG GCT GCT CAG GGC GAT ATT 136  
Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp Ile  
5 10 15

ACT GCA CCC GGC GGT GCT CGC CGT TTA ACG GGT GAT CAG ACT GCC 181  
Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala  
20 25 30

40    GCT CTG CGT GAT TCT CTT AGC GAT AAA CCT GCA AAA AAT ATT ATT 226  
      Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile  
                35                      40                      45

45      TTG CTG ATT GGC GAT GGG ATG GGG GAC TCG GAA ATT ACT GCC GCA 271  
Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala

50                          55                          60

5	CGT AAT TAT GCC GAA GGT GCG GGC GGC TTT TTT AAA GGT ATA GAT 316 Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp 65 70 75
10	GCC TTA CCG CTT ACC GGG CAA TAC ACT CAC TAT GCG CTG AAT AAA 361 Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys 80 85 90
15	AAA ACC GGC AAA CCG GAC TAC GTC ACC GAC TCG GCT GCA TCA GCA 406 Lys Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala 95 100 105
20	ACC GCC TGG TCA ACC GGT GTC AAA ACC TAT AAC GGC GCG CTG GGC 451 Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly 110 115 120
25	GTC GAT ATT CAC GAA AAA GAT CAC CCA ACG ATT CTG GAA ATG GCA 496 Val Asp Ile His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala 125 130 135
30	AAA GCC GCA GGT CTG GCG ACC GGT AAC GTT TCT ACC GCA GAG TTG 541 Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu 140 145 150
35	CAG GAT GCC ACG CCC GCT GCG CTG GTG GCA CAT GTG ACC TCG CGC 586 Gln Asp Ala Thr Pro Ala Ala Leu Val Ala His Val Thr Ser Arg 155 160 165
40	AAA TGC TAC GGT CCG AGC GCG ACC AGT GAA AAA TGT CCG GGT AAC 631 Lys Cys Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly Asn 170 175 180
45	GCT CTG GAA AAA GGC GGA AAA GGA TCG ATT ACC GAA CAG CTG CTT 676 Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu 185 190 195
50	AAC GCT CGT GCC GAC GTT ACG CTT GGC GGC GGC GCA AAA ACC TTT 721 Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe 200 205 210
55	GCT GAA ACG GCA ACC GCT GGT GAA TGG CAG GGA AAA ACG CTG CGT 766 Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg 215 220 225
60	GAA CAG GCA CAG GCG CGT GGT TAT CAG TTG GTG AGC GAT GCT GCC 811 Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp Ala Ala 230 235 240
65	TCA CTG AAT TCG GTG ACG GAA GCG AAT CAG CAA AAA CCC CTG CTT 856 Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu Leu 245 250 255
70	GGC CTG TTT GCT GAC GGC AAT ATG CCA GTG CGC TGG CTA GGA CCG 901 Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro 260 265 270
75	AAA GCA ACG TAC CAT GGC AAT ATC GAT AAG CCC GCA GTC ACC TGT 946 Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys 275 280 285

ACG CCA AAT CCG CAA CGT AAT GAC AGT GTA CCA ACC CTG GCG CAG 991  
 Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln  
 290 295 300

5 ATG ACC GAC AAA GCC ATT GAA TTG TTG AGT AAA AAT GAG AAA GGC 1036  
 Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly  
 305 310 315

10 TTT TTC CTG CAA GTT GAA GGT GCG TCA ATC GAT AAA CAG GAT CAT 1081  
 Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His  
 320 325 330

15 GCT GCG AAT CCT TGT GGG CAA ATT GGC GAG ACG GTC GAT CTC GAT 1126  
 Ala Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp  
 335 340 345

20 GAA GCC GTA CAA CGG GCG CTG GAA TTC GCT AAA AAG GAG GGT AAC 1171  
 Glu Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn  
 350 355 360

25 ACG CTG GTC ATA GTC ACC GCT GAT CAC GCC CAC GCC AGC CAG ATT 1216  
 Thr Leu Val Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile  
 365 370 375

GTT GCG CCG GAT ACC AAA GCT CCG GGC CTC ACC CAG GCG CTA AAT 1261  
 Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn  
 380 385 390

30 ACC AAA GAT GGC GCA GTG ATG GTG ATG AGT TAC GGG AAC TCC GAA 1306  
 Thr Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly Asn Ser Glu  
 395 400 405

35 GAG GAT TCA CAA GAA CAT ACC GGC AGT CAG TTG CGT ATT GCG GCG 1351  
 Glu Asp Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile Ala Ala  
 410 415 420

40 TAT GGC CCG CAT GCC GCC AAT GTT GTT GGA CTG ACC GAC CAG ACC 1396  
 Tyr Gly Pro His Ala Ala Asn Val Val Gly Leu Thr Asp Gln Thr  
 425 430 435

45 GAT CTC TTC TAC ACC ATG AAA GCC GCT CTG GGG CTG AAA CCG CCT 1441  
 Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly Leu Lys Pro Pro  
 440 445 450

AGC GCT GAC GTG TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA 1486  
 Ser Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro  
 455 460 465

50 GTC GAC AAC TTC GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG CAG 1531  
 Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln  
 470 475 480

55 GTC GCC GCG TAC CCC GAT CAT ATT ACG AAG TAC GGA AAG TGC GGA 1576  
 Val Ala Ala Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly  
 485 490 495

60 TGG GCT GAG TAC ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG CGC 1621  
 Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg  
 500 505 510

TAC TCT GTA ATC CAC GGC AAG GAA TAC TTT TCC GAA GGT ACC GCC 1666  
 Tyr Ser Val Ile His Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala  
 515 520 525

5 TAC CCA GTT GGT GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC TAC 1711  
 Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Tyr  
 530 535 540

10 ACT ATT GGA GGT GTG ACC CAG GAG GGT GTA TTC AAC GTA CTC TCC 1756  
 Thr Ile Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val Leu Ser  
 545 550 555

15 ACT GAC AAC AAG AAC TAC ATC ATC GGA TAC TTT TGC TCG TAC GAC 1801  
 Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp  
 560 565 570

20 GAG GAC AAG AAG GGA CAC ATG GAC TTG GTC TGG GTG CTC TCC AGA 1846  
 Glu Asp Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg  
 575 580 585

25 AGC ATG GTC CTT ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC 1891  
 Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr  
 590 595 600

CTT ATC GGC TCC CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT 1936  
 Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser  
 605 610 615

30 GAC TTC TCT GAA GCC GCC TGC AAG GTC AAC AAT AGC AAC TGG TCT 1981  
 Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser  
 620 625 630

35 CAC CCG CAG TTC GAA AAA TAATAAGCTT 2009  
 His Pro Gln Phe Glu Lys  
 635

<210> 18  
 40 <211> 2005 bases pairs  
 <212> DNA  
 <213> fragment of plasmid PBBP29

<220>  
 45 <221> sig\_peptide  
 <222> (22)...(84)

<220>  
 <221> mat\_peptide  
 50 <222> (85)...(1998)

<223> fusion protein of mutein DigA16, Strep-Tag II, linker peptide Gly(5) and alkaline phosphatase

<220>

5 <221> CDS

<222> (85)...(606)

<223> mutein DigA16

<220>

10 <221> CDS

<222> (607)...(636)

<223> Strep-Tag II affinity tag

<220>

15 <221> CDS

<222> (637)...(651)

<223> linker peptide Gly-Gly-Gly-Gly-Gly

<220>

20 <221> CDS

<222> (652)...(1998)

<223> alkaline phosphatase without signalling sequence and N-terminal Arg

<400> 18

25

TCTAGATAAC GAGGGCAAAA A ATG AAA AAG ACA GCT ATC GCG ATT 45  
Met Lys Lys Thr Ala Ile Ala Ile  
-21 -20 -15

30

GCA GTG GCA CTG GCT GGT TTC GCT ACC GTA GCG CAG GCC GAC GTG 90  
Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val  
-10 -5 -1 1

35

TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA GTC GAC AAC TTC 135  
Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe  
5 10 15

40

GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG CAG GTC GCC GCG TAC 180  
Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr  
20 25 30

CCC GAT CAT ATT ACG AAG TAC GGA AAG TGC GGA TGG GCT GAG TAC 225  
Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr  
35 40 45

45

23

	ACT	CCT	GAA	GGC	AAG	AGT	GTC	AAA	GTT	TCG	CGC	TAC	TCT	GTA	ATC	270
	Thr	Pro	Glu	Gly	Lys	Ser	Val	Lys	Val	Ser	Arg	Tyr	Ser	Val	Ile	
			50					55					60			
5	CAC	GGC	AAG	GAA	TAC	TTT	TCC	GAA	GGT	ACC	GCC	TAC	CCA	GTT	GGT	315
	His	Gly	Lys	Glu	Tyr	Phe	Ser	Glu	Gly	Thr	Ala	Tyr	Pro	Val	Gly	
			65					70					75			
10	GAC	TCC	AAG	ATT	GGA	AAG	ATC	TAC	CAC	AGC	TAC	ACT	ATT	GGA	GGT	360
	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	His	Ser	Tyr	Thr	Ile	Gly	Gly	
			80					85					90			
15	GTG	ACC	CAG	GAG	GGT	GTA	TTC	AAC	GTA	CTC	TCC	ACT	GAC	AAC	AAG	405
	Val	Thr	Gln	Glu	Gly	Val	Phe	Asn	Val	Leu	Ser	Thr	Asp	Asn	Lys	
			95					100					105			
20	AAC	TAC	ATC	ATC	GGA	TAC	TTT	TGC	TCG	TAC	GAC	GAG	GAC	AAG	AAG	450
	Asn	Tyr	Ile	Ile	Gly	Tyr	Phe	Cys	Ser	Tyr	Asp	Glu	Asp	Lys	Lys	
			110					115					120			
25	GGA	CAC	ATG	GAC	TTG	GTC	TGG	GTG	CTC	TCC	AGA	AGC	ATG	GTC	CTT	495
	Gly	His	Met	Asp	Leu	Val	Trp	Val	Leu	Ser	Arg	Ser	Met	Val	Leu	
			125					130					135			
30	ACT	GGT	GAA	GCC	AAG	ACC	GCT	GTC	GAG	AAC	TAC	CTT	ATC	GGC	TCC	540
	Thr	Gly	Glu	Ala	Lys	Thr	Ala	Val	Glu	Asn	Tyr	Leu	Ile	Gly	Ser	
			140					145					150			
35	CCA	GTA	GTC	GAC	TCC	CAG	AAA	CTG	GTA	TAC	AGT	GAC	TTC	TCT	GAA	585
	Pro	Val	Val	Asp	Ser	Gln	Lys	Leu	Val	Tyr	Ser	Asp	Phe	Ser	Glu	
			155					160					165			
40	GCC	GCC	TGC	AAG	GTC	AAC	AAT	AGC	AAC	TGG	TCT	CAC	CCG	CAG	TTC	630
	Ala	Ala	Cys	Lys	Val	Asn	Asn	Ser	Asn	Trp	Ser	His	Pro	Gln	Phe	
			170					175					180			
45	GAA	AAA	GGT	GGC	GGC	GGT	GGT	ACA	CCA	GAA	ATG	CCT	GTT	CTG	GAA	675
	Glu	Lys	Gly	Gly	Gly	Gly	Gly	Thr	Pro	Glu	Met	Pro	Val	Leu	Glu	
			185					190					195			
50	AAC	CGG	GCT	GCT	CAG	GGC	GAT	ATT	ACT	GCA	CCC	GGC	GGT	GCT	CGC	720
	Asn	Arg	Ala	Ala	Gln	Gly	Asp	Ile	Thr	Ala	Pro	Gly	Gly	Ala	Arg	
			200					205					210			
55	CGT	TTA	ACG	GGT	GAT	CAG	ACT	GCC	GCT	CTG	CGT	GAT	TCT	CTT	AGC	765
	Arg	Leu	Thr	Gly	Asp	Gln	Thr	Ala	Ala	Leu	Arg	Asp	Ser	Leu	Ser	
			215					220					225			
60	GAT	AAA	CCT	GCA	AAA	AAT	ATT	ATT	TTG	CTG	ATT	GGC	GAT	GGG	ATG	810
	Asp	Lys	Pro	Ala	Lys	Asn	Ile	Ile	Leu	Leu	Ile	Gly	Asp	Gly	Met	
			230					235					240			
65	GGG	GAC	TCG	GAA	ATT	ACT	GCC	GCA	CGT	AAT	TAT	GCC	GAA	GGT	GCG	855
	Gly	Asp	Ser	Glu	Ile	Thr	Ala	Ala	Arg	Asn	Tyr	Ala	Glu	Gly	Ala	
			245					250					255			
70	GGC	GGC	TTT	TTT	AAA	GGT	ATA	GAT	GCC	TTA	CCG	CTT	ACC	GGG	CAA	900
	Gly	Gly	Phe	Phe	Lys	Gly	Ile	Asp	Ala	Leu	Pro	Leu	Thr	Gly	Gln	
			260					265					270			

	TAC	ACT	CAC	TAT	GCG	CTG	AAT	AAA	AAA	ACC	GGC	AAA	CCG	GAC	TAC	945
	Tyr	Thr	His	Tyr	Ala	Leu	Asn	Lys	Lys	Thr	Gly	Lys	Pro	Asp	Tyr	
			275					280					285			
5	GTC	ACC	GAC	TCG	GCT	GCA	TCA	GCA	ACC	GCC	TGG	TCA	ACC	GGT	GTC	990
	Val	Thr	Asp	Ser	Ala	Ala	Ser	Ala	Thr	Ala	Trp	Ser	Thr	Gly	Val	
			290					295					300			
10	AAA	ACC	TAT	AAC	GGC	GCG	CTG	GGC	GTC	GAT	ATT	CAC	GAA	AAA	GAT	1035
	Lys	Thr	Tyr	Asn	Gly	Ala	Leu	Gly	Val	Asp	Ile	His	Glu	Lys	Asp	
			305					310					315			
15	CAC	CCA	ACG	ATT	CTG	GAA	ATG	GCA	AAA	GCC	GCA	GGT	CTG	GCG	ACC	1080
	His	Pro	Thr	Ile	Leu	Glu	Met	Ala	Lys	Ala	Ala	Gly	Leu	Ala	Thr	
			320					325					330			
20	GGT	AAC	GTT	TCT	ACC	GCA	GAG	TTG	CAG	GAT	GCC	ACG	CCC	GCT	GCG	1125
	Gly	Asn	Val	Ser	Thr	Ala	Glu	Leu	Gln	Asp	Ala	Thr	Pro	Ala	Ala	
			335					340					345			
25	CTG	GTG	GCA	CAT	GTG	ACC	TCG	CGC	AAA	TGC	TAC	GGT	CCG	AGC	GCG	1170
	Leu	Val	Ala	His	Val	Thr	Ser	Arg	Lys	Cys	Tyr	Gly	Pro	Ser	Ala	
			350					355					360			
30	ACC	AGT	GAA	AAA	TGT	CCG	GGT	AAC	GCT	CTG	GAA	AAA	GGC	GGA	AAA	1215
	Thr	Ser	Glu	Lys	Cys	Pro	Gly	Asn	Ala	Leu	Glu	Lys	Gly	Gly	Lys	
			365					370					375			
35	GGA	TCG	ATT	ACC	GAA	CAG	CTG	CTT	AAC	GCT	CGT	GCC	GAC	GTT	ACG	1260
	Gly	Ser	Ile	Thr	Glu	Gln	Leu	Leu	Asn	Ala	Arg	Ala	Asp	Val	Thr	
			380					385					390			
40	CTT	GGC	GGC	GGC	GCA	AAA	ACC	TTT	GCT	GAA	ACG	GCA	ACC	GCT	GGT	1305
	Leu	Gly	Gly	Gly	Ala	Lys	Thr	Phe	Ala	Glu	Thr	Ala	Thr	Ala	Gly	
			395					400					405			
45	GAA	TGG	CAG	GGA	AAA	ACG	CTG	CGT	GAA	CAG	GCA	CAG	GCG	CGT	GGT	1350
	Glu	Trp	Gln	Gly	Lys	Thr	Leu	Arg	Glu	Gln	Ala	Gln	Ala	Arg	Gly	
			410					415					420			
50	TAT	CAG	TTG	GTG	AGC	GAT	GCT	GCC	TCA	CTG	AAT	TCG	GTG	ACG	GAA	1395
	Tyr	Gln	Leu	Val	Ser	Asp	Ala	Ala	Ser	Leu	Asn	Ser	Val	Thr	Glu	
			425					430					435			
55	GCG	AAT	CAG	CAA	AAA	CCC	CTG	CTT	GGC	CTG	TTT	GCT	GAC	GGC	AAT	1440
	Ala	Asn	Gln	Gln	Lys	Pro	Leu	Leu	Gly	Leu	Phe	Ala	Asp	Gly	Asn	
			440					445					450			
60	ATG	CCA	GTG	CGC	TGG	CTA	GGA	CCG	AAA	GCA	ACG	TAC	CAT	GGC	AAT	1485
	Met	Pro	Val	Arg	Trp	Leu	Gly	Pro	Lys	Ala	Thr	Tyr	His	Gly	Asn	
			455					460					465			
65	ATC	GAT	AAG	CCC	GCA	GTC	ACC	TGT	ACG	CCA	AAT	CCG	CAA	CGT	AAT	1530
	Ile	Asp	Lys	Pro	Ala	Val	Thr	Cys	Thr	Pro	Asn	Pro	Gln	Arg	Asn	
			470					475					480			
70	GAC	AGT	GTA	CCA	ACC	CTG	GCG	CAG	ATG	ACC	GAC	AAA	GCC	ATT	GAA	1575
	Asp	Ser	Val	Pro	Thr	Leu	Ala	Gln	Met	Thr	Asp	Lys	Ala	Ile	Glu	
			485					490					495			





P 2305945

Atty. Dkt. No. 029029-0101

DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I HEREBY DECLARE:

name; THAT my residence, post office address, and citizenship are as stated below next to my

below) or an original, first, and sole inventor (if only one inventor is named below or in an attached Declaration) of the subject matter which is claimed and for which a patent is sought on the invention entitled

MUTAINS OF THE BILIN-BINDING PROTEIN

(Attorney Docket No. 029029-0101)

the specification of which (check one)

is attached hereto.

X was filed on June 8, 2000 as United States Application Number or PCT International Application Number PCT/DE00/01873 and was amended on (if applicable).

THAT I do not know and do not believe that the same invention was ever known or used by others in the United States of America, or was patented or described in any printed publication in any country, before I (we) invented it;

THAT I do not know and do not believe that the same invention was patented or described in any printed publication in any country, or in public use or on sale in the United States of America, for more than one year prior to the filing date of this United States application;

THAT I do not know and do not believe that the same invention was first patented or made the subject of an inventor's certificate that issued in any country foreign to the United States of America before the filing date of this United States application if the foreign application was filed by me (us), or by my (our) legal representatives or assigns, more than twelve months (six months for design patents) prior to the filing date of this United States application;

THAT I have reviewed and understand the contents of the above-identified specification, including the claim(s), as amended by any amendment specifically referred to above;

THAT I believe that the above-identified specification contains a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention, and sets forth the best mode contemplated by me of carrying out the invention; and

THAT I acknowledge the duty to disclose to the U.S. Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56.

002.676627.1

Page 1 of 3

NR.292 S.2

18.FEB.2002 11:40 VJP MUNICH

I HEREBY CLAIM foreign priority benefits under Title 35, United States Code § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT international application which designated at least one country other than the United States of America, listed below and have also identified below any foreign application for patent or inventor's certificate or of any PCT international application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application Number	Country	Foreign Filing Date	Priority Claimed?	Certified Copy Attached?
199 26 068.0	Germany	June 8, 1999	YES	

I HEREBY CLAIM the benefit under Title 35, United States Code § 119(e) of any United States provisional application(s) listed below.

U.S. Provisional Application Number	Filing Date

I HEREBY CLAIM the benefit under Title 35, United States Code, § 120 of any United States application(s), or § 365(c) of any PCT international application designating the United States of America, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT international application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application.

U.S. Parent Application Number	PCT Parent Application Number	Parent Filing Date	Parent Patent Number

I HEREBY APPOINT the registered attorneys and agents at Customer Number 22428



22428

PATENT TRADEMARK OFFICE

to have full power to prosecute this application and any continuations, divisions, reissues, and reexaminations thereof, to receive the patent, and to transact all business in the United States Patent and Trademark Office connected therewith.

I request that all correspondence be directed to:

Stephen B. Maebius  
FOLEY & LARDNER  
Customer Number: 22428



22428  
PATENT TRADEMARK OFFICE

Telephone: (202) 672-5569  
Facsimile: (202) 672-5399

I UNDERSTAND AND AGREE THAT the foregoing attorneys and agents appointed by me to prosecute this application do not personally represent me or my legal interests, but instead represent the interests of the legal owner(s) of the invention described in this application.

I FURTHER DECLARE THAT all statements made herein of my own knowledge are true, and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Name of first inventor  
Residence  
Citizenship  
Post Office Address  
Inventor's signature  
Date

Steffen SCHLEHUBER

Freising, Germany

German

Mustr. 21 21

D-85356, Freising, Germany

X Schlehuber

X 30.01.2002